

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SOURCE	mice hybridoma cells.
ORGANISM	Mus sp.
	Unclassified.

## ALIGNMENTS

Result No.	Score	Match	Query Length	DB ID	Description	Pred. No.
1	354	92.9	381	59	S50261	Ig VL-anti-CD4 mAb M-0.00e+00
2	352	92.9	393	56	MUS1VJR	Mus musculus germline0.00e+00
3	352	92.4	395	56	MUS1GKAAAL	Mouse Ig kappa chain0.00e+00
4	350	91.9	381	14	MM16689	Mus musculus Ig light0.00e+00
5	350	91.9	381	82	MMU16689	Mus musculus Ig light0.00e+00
6	344	90.3	381	54	MMU05217	Mus musculus Balb/c a0.00e+00
7	343	90.0	378	56	MUS1GK527A	Mus musculus (clone 50.00e+00
8	338	88.2	366	56	MUS1GKCKKO	Mouse Ig kappa-chain0.00e+00
9	328	86.1	345	56	MUS1GKCPW	Mouse Ig active kappa0.00e+00
10	316	82.9	395	56	MUS1GKAAAM	Mouse Ig kappa chain0.00e+00
11	310	81.4	324	56	MUS1GKAVD	Mouse Ig rearranged k0.00e+00
12	310	81.4	324	54	MM1GKL229	M.musculus gene for i0.00e+00
13	310	81.4	324	54	MM1GKL38	M.musculus gene for i0.00e+00
14	310	81.4	324	54	MM1GKL233	M.musculus gene for i0.00e+00
15	310	81.4	324	56	MUS1GKAVE	Mouse Ig rearranged k0.00e+00
16	310	81.4	324	56	MUS1GKAVE	Mouse Ig rearranged k0.00e+00
17	308	80.8	408	59	S63022	anti-ganglioside CD30.00e+00
18	302	79.3	508	53	MHS57HVL	M.musculus/ H.sapiens4.71e-300
19	298	78.2	324	54	MM1GCL151	M.musculus mRNA for I1.68e-295
20	298	78.2	324	54	MM1GKLAB0	M.musculus gene for i1.68e-295
21	298	78.2	324	54	MM1GKLAC1	M.musculus gene for i1.68e-295
22	298	78.2	324	56	MUS1GKAVA	Mouse Ig rearranged k1.68e-295
23	298	78.2	324	56	MUS1GKAVH	Mouse Ig rearranged k1.68e-295
24	298	78.2	324	54	MM1GKL218	M.musculus gene for i1.68e-295
25	298	78.2	324	56	MUS1GKAVJ	Mouse Ig rearranged k1.68e-295
26	296	77.7	330	54	MMU20820	Mus musculus Ig Fab F3.18e-293
27	295	77.4	331	54	MMU1AH10	M.musculus NL4H10 mRN4.37e-292
28	294	77.2	321	56	MUS1GKNJ	Mouse Ig kappa germli6.00e-291
29	294	77.2	321	56	MUS1GKADT	Mouse Ig rearranged k6.00e-291
30	294	77.2	323	54	MM1GKV36	Mouse hybridoma 36-656.00e-291
31	294	77.2	323	56	MUS1GKABT	Mouse Ig kappa-chain6.00e-291
32	294	77.2	324	56	MUS1GKCKD	Mouse Ig active kappa6.00e-291
33	294	77.2	324	56	MUS1GKAVC	Mouse Ig rearranged k6.00e-291
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36	294	77.2	324	54	MM1GKL228	M.musculus gene for i6.00e-291
37	294	77.2	324	56	MUS1GKCRR	Mouse Ig kappa-chain6.00e-291
38	294	77.2	324	56	MUS1GKCB0	Mouse Ig active kappa6.00e-291
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42	293	76.9	324	56	MUS1GKCRK	Mouse Ig kappa-chain8.23e-290
43	293	76.9	324	56	MUS1GKCRQ	Mouse Ig kappa-chain8.23e-290
44	292	76.6	321	53	MUS1GGLAQ	Mouse Ig light-chain1.13e-288
45	292	76.6	324	53	MM1GKLS6R	M.musculus gene for i1.13e-288

RESULT	1
LOCUS	S50261
DEFINITION	Ig VJ-anti-CD4 mAb W-1151 variable region light chain [J2, chimeric antibody] [mice, hybridoma cells. mRNA Partial. 381 nt].
	381 bp mRNA ROD 02-APR-1993



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	Best local Similarity	96.3%; Pred. No. 0.00e+00;
	Matches	366; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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Qy	1 ATGGTGTCTCAGCTCAGTTCCTCGGTCCTCGTGCTGCTGTTTCAAGGTACCATGT	60             
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Db	132 atcagttgcaggccaagtcaggacattagcaattattaaacttgttatcacgagaacca	191             
Qy	121 ATCAGTTGCCAGGCCAAGTCAGGACATTAGCAGTTATTTAAACTGGGTATCAGCAGAACC	180             
Db	192 gatgaacctgttaaactcctgatctactaacatacatattacaactcaggagtcgccagca	251             
Qy	181 GATGGAACATTAAACTCCTGATCTACTACATCATCAAGATTACACTCAGGAGTCCCATCA	240             
Db	252 aggttcagtgccagtggtgtcggaacagattattctctcatcattagcaacctggagcaa	311             
Qy	241 AGGTTCACTGGCAGTGGCTCGAACAGATTATCTCTCACCATTAAACAACCTGGAGCAA	300             
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Qy	301 GAAGACATTCGCCACTTACTTTTGGCAACGGTAACAGCTTCGCTACACGTCGAGGG	360             
Db	372 gggtcccaagctggaaataaa	391             
Qy	361 GGGACCAAGCTGGAAATAAA	380             
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ID	MM16689	standard; RNA; ROD; 381 BP.
AC	U16689;	
DT	03-NOV-1995 (Rel. 45, Created)	
DT	03-NOV-1995 (Rel. 45, Last updated, Version 1)	
DE	Mus musculus Ig light chain leader and variable region VK V gene	
DE	family mRNA, partial cds.	
KW	.	
OS	Mus musculus (mouse)	
OC	Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;	
OC	Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.	
RN	[1]	
RP	1-381	
RA	White K.D., Frank M.B., Foundling S., Cummings R.D., Waxman F.J.;	
RT	"Effect of variable domain structure and CH2-linked carbohydrate	
RT	on C3b and C4b deposition and classical complement pathway	
RT	activation by immunoglobulins";	
RL	Unpublished.	
RL	[2]	
RP	1-381	
RA	Frank B.;	
RT	,	
RL	Submitted (27-OCT-1994) to the ENBL/GenBank/DBJ databases.	
RL	Bart Frank, Arthritis and Immunology Program, Oklahoma Medical	
RL	Research Foundation, 825 NE 13th Street, Oklahoma City, OK 73104,	
RL	USA	
CC	NCBI gi: 1041800	
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FT      61..324
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FT      61..381
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Matches 365; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy 61 GATATCCAGATGACACAGACTACATCTCCTCTGTCTGCTCTCTGGGACACAGATCACC 120  
  
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Qy 181 GATGGAACATTATTAACCTCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240  
  
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Qy 301 GAACAATTGGCACTTACTTTTGGCAACAGGGTAACACGGTTCCTCGTACACGTTTCGGAAGG 360  
  
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Qy 361 GGGACCAAGCTGGAAATAAA 380

RESULT	5
LOCUS	MMU1689      381 bp    mRNA                  ROD         28-OCT-1995
DEFINITION	Mus musculus Ig light chain leader and variable region Vk V gene family mRNA, partial cds.
ACCESSION	U16689
KEYWORDS	.
SOURCE	mouse.
ORGANISM	Mus musculus
Eukaryotes; Mitochondria; Eukaryote crown group; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia;	

REFERENCE	Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrastoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus.
AUTHORS	1 (bases 1 to 381) White,K.D., Frank,M.B., Foundling,S., Cummings,R.D. and Waxman,F.J.
TITLE	Effect of variable domain structure and CH2-linked carbohydrate on C3b and C4b deposition and classical complement pathway activation by immunoglobulins
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 381)
AUTHORS	Frank, B.
TITLE	Direct Submission
JOURNAL	Submitted (27-OCT-1994) Bart Frank, Arthritis and Immunology Program, Oklahoma Medical Research Foundation, 825 NE 13th Street, Oklahoma City, OK 73104, USA
COMMENT	NCBI gi: 1041800
FEATURES	Location/Qualifiers 1..381 source

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immunizations"

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V_region	61..381	/note="member of the murine Vk V gene family"
J_segment	346..381	/product="immunoglobulin light chain variable region"
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BASE COUNT	105 a 92 c 83 g 101 t	
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Query Match	91.9%;	Score 350;	DB 82;	Length 381;
Best Local Similarity	96.1%;	Pred. No. 0.00e+00;		
Matches	365;	Conservative 0;	Mismatches 15;	Indels 0; Gaps 0;
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Qy	121	ATCAGTTGCAGGCAAGTCAGGACATTAGCAGGTATTTTAAACTGGTATCAGCAAGAAACA	180	
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9

Db 241 aggttcagtcagtcgggtcggagacagattattctctcaccattagacaacctggagcaaa 300  
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RESULT 6  
LOCUS MM005217 381 bp mRNA ROD 20-MAY-1994  
DEFINITION Mus musculus Balb/c anti-platelet integrin gpIIb/IIIa light chain  
immunoglobulin, partial cds.  
ACCESSION U05217  
KEYWORDS  
SOURCE mouse.  
ORGANISM Mus musculus  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Rodentia; Myomorpha; Muridae; Mus.

REFERENCE 1 (sites)  
AUTHORS Co,M., Yano,S., Heu,R.K., Landolfi,N.F., Vasquez,M., Cole,M.S.,  
Tso,J.T., Bringman,T., Laird,W., Hudson,D., Kawamura,K. and  
Suzuki,K.

TITLE A humanized antibody specific for the platelet integrin gpIIb/IIIa  
JOURNAL J. Immunol. 152, 2968-2976 (1994)  
MEDLINE 94194058  
REFERENCE 2 (bases 1 to 381)  
AUTHORS Co,M.

TITLE Direct Submission  
JOURNAL Submitted (14-JUN-1994) Man Sung Co, Protein Design Labs., Inc.,  
2375 Garcia Ave, Mountain View, CA 94043, USA  
COMMENT NCBI gi: 460600

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Db 61 gatattccagatgacacagactacatccctcctgtcctctcctctcctctcctcagcagatcacc 120

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RESULT 7  
LOCUS MUSIGK527A 378 bp mRNA ROD 25-JAN-1995  
DEFINITION Mus musculus (clone 5-27) anti-fluorescein antibody (IgK) mRNA,  
V-region.

ACCESSION L39092  
KEYWORDS V-region; V-segment; anti-fluorescein antibody;  
immunoglobulin kappa-chain; monoclonal antibody.

SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) hybridoma cDNA  
to mRNA.

ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (sites)  
AUTHORS Bedzyk,W.D., Herron,J.N., Edmundson,A.B. and Voss,E.W. Jr.

TITLE Active site structure and antigen binding properties of  
idiotypically cross-reactive anti-fluorescein monoclonal antibodies  
J. Biol. Chem. 265 (1), 133-138 (1990)

JOURNAL 90094387

MEDLINE

COMMENT NCBI gi: 639666

FEATURES Location/Qualifiers

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JOURNAL different antigen (phoxazalone, NP or GAT)  
MEDLINE Mol. Immunol. 25, 859-865 (1988)  
COMMENT 89096973  
FEATURES NCBI gi: 197161 Location/Qualifiers  
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RESULT 10  
LOCUS MUSICKRAM 395 bp mRNA ROD 29-OCT-1994  
DEFINITION Mouse Ig kappa chain mRNA V-J region, 5' end.  
ACCESSION M60020  
KEYWORDS C-region; J-region; V-region; immunoglobulin light chain;  
immunoglobulin-kappa.  
SOURCE Mouse (strain C57BL/6) spleen cell hybridoma 222, cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 395)  
AUTHORS Brigido, M.M. and Stollar, B.D.

TITLE Two induced anti-2-DNA monoclonal antibodies use VH gene segments  
related to those of anti-DNA autoantibodies  
JOURNAL J. Immunol. 146 (6), 2005-2009 (1991)  
MEDLINE 91170743  
COMMENT NCBI gi: 196425 Location/Qualifiers  
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Qy 121 ATCAGTTGACGGGCAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACCA 180  
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Qy 241 AGGTTCAAGTGGCAGTGGGTCTGGAAACAGATTATTCTCTCACCATTAAACACCTGGAGCA 300  
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REFERENCE 2 (bases 1 to 324)  
AUTHORS Wysocki,L.J., Crendon,G., Lehmann,K.R. and Cambier,J.C.  
TITLE B-cell proliferation initiated by Ia cross-linking and sustained by interleukins leads to class switching but not somatic mutation in vitro

JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 324)  
AUTHORS Wysocki,L.J., Creadon,G., Lehmann,K.R. and Cambier,J.C.  
TITLE B-cell proliferation initiated by Ia cross-linking and sustained by interleukins leads to class switching but not somatic mutation in vitro

JOURNAL Immunology 75 (1), 116-121 (1992)  
MEDLINE 92165291  
COMMENT NCBI gi: 511029  
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Best Local Similarity 98.4%; Pred. No. 0.00e+00;  
Matches 315; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 301 gggaccaagctggaaataaa 320  
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Qy 361 GGGACCAAGCTGGAATAAA 380  
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RESULT 13  
LOCUS MWIGKL38 324 bp DNA ROD 05-NOV-1994  
DEFINITION M.musculus gene for immunoglobulin kappa light chain variable

region (KL3.8).  
X55046  
KEYWORDS immunoglobulin kappa light chain.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Vertebrata; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 324)  
AUTHORS Wysocki,L.J.  
TITLE Direct Submission  
JOURNAL Submitted (14-JAN-1991) to the EMBL/GenBank/DBJ databases. L.J. Wysocki, NATIONAL JEWISH CENTER FOR IMMUNOLOGY AND RESPIRATORY MEDICINE, DEPT OF PEDIATRICS K902, 1400 JACKSON ST, DENVER CO 80206, USA

REFERENCE 2 (bases 1 to 324)  
AUTHORS Wysocki,L.J., Crendon,G., Lehmann,K.R. and Cambier,J.C.  
TITLE B-cell proliferation initiated by Ia cross-linking and sustained by interleukins leads to class switching but not somatic mutation in vitro

JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 324)  
AUTHORS Wysocki,L.J., Creadon,G., Lehmann,K.R. and Cambier,J.C.  
TITLE B-cell proliferation initiated by Ia cross-linking and sustained by interleukins leads to class switching but not somatic mutation in vitro

JOURNAL Immunology 75 (1), 116-121 (1992)  
MEDLINE 92165291  
COMMENT NCBI gi: 511033  
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misc\_feature 285..324  
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BASE COUNT 98 a 78 c 72 g 76 t  
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Query Match 81.4%; Score 310; DB 54; Length 324;  
Best Local Similarity 98.4%; Pred. No. 0.00e+00;  
Matches 315; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DEFINITION M.musculus gene for immunoglobulin kappa light chain variable
region (KL2.33).
ACCESSION X55045
KEYWORDS immunoglobulin kappa light chain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Euthera; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 324)
Wysocki, L.J.
Direct Submission
Submitted (14-JAN-1991) to the EMBL/GenBank/DBJ databases. L.J.
Wysocki, NATIONAL JEWISH CENTER FOR IMMUNOLOGY AND RESPIRATORY
MEDICINE, DEPT OF PEDIATRICS K902, 1400 JACKSON ST, DENVER CO
80206, USA
2 (bases 1 to 324)
Wysocki, L.J., Crendon, G., Lehmann, K.R. and Cambier, J.C.
B-cell proliferation initiated by Ia cross-linking and sustained by
interleukins leads to class switching but not somatic mutation in
vitro
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 324)
Wysocki, L.J., Creadon, G., Lehmann, K.R. and Cambier, J.C.
B-cell proliferation initiated by Ia cross-linking and sustained by
interleukins leads to class switching but not somatic mutation in
vitro
JOURNAL Immunology 75 (1), 116-121 (1992)
MEDLINE 92165291
COMMENT NCBI gi: 511031
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Best Local Similarity 98.4%; Pred. No. 0.00e+00;
Matches 315; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 1 qatatccagatgacacagactacatctcctgtctgcctctctgggaacagagtcacc 60
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Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAACTGCTATCAGCAGAAACCA 180
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Db 121 gatggaactgttaacctcctgatctactacatcaagaattacactcaggagtcaccatca 180
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Qy 181 GATGGAACATTATAAAGCTCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
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Db 181 aggttcagtcgagtcggttcggaacagagattattctctcaccattagcaaccttgagcaa 240
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Db 301 gggaccaagctggaataaaa 320
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Qy 361 GGGACCAAGCTGGAATAAA 380
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RESULT 15
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DEFINITION Mouse Ig rearranged kappa-chain (V-IdCR J2) gene V10-J region,
hybridoma KL3.8, partial cds.
ACCESSION M63613
KEYWORDS V-region; immunoglobulin light chain; kappa chain;
processed gene.
SOURCE Mus musculus (strain (CAL-20 x A/J) F1) B lymphocyte DNA.
ORGANISM Mus musculus
Eukaryotes; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Euthera; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (sites)
AUTHORS Sakano, H., Huppi, K., Heinrich, G. and Tonegawa, S.
TITLE Sequences at the somatic recombination sites of immunoglobulin
light-chain genes
JOURNAL Nature 280 (5720), 288-294 (1979)
MEDLINE 79221879
REFERENCE 2 (sites)
AUTHORS Wysocki, L.J., Gridley, T., Huang, S., Grandea, A.G. III. and
Geffer, M.L.
TITLE Single germline VH and V kappa genes encode predominating antibody
variable regions elicited in strain A mice by immunization with
P-azophenylarsenate
JOURNAL J. Exp. Med. 166 (1), 1-11 (1987)
MEDLINE 87252903
REFERENCE 3 (bases 1 to 324)
AUTHORS Wysocki, L.J., Creadon, G., Lehmann, K.R. and Cambier, J.C.
TITLE B-cell proliferation initiated by Ia cross-linking and sustained by
interleukins leads to class switching but not somatic mutation in
vitro
JOURNAL Immunology 75 (1), 116-121 (1992)
MEDLINE 92165291
COMMENT NCBI gi: 196788
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Search completed: Mon Jul 8 08:52:40 1996  
Job time : 271 secs.









DT	04-MAR-1993	(first entry)	
DE	ME4 Light Chain V Region (mouse).		
KW	Monoclonal antibody; chimera; light; heavy; chain; constant;		
KW	variable; antigen; diagnosis; cancer; tumour; ss.		
OS	Mus musculus.		
FS			
FT	Key	Location/Qualifiers	
FT	CD5	61..444	
FT	/*tag= a		
PN	W09002569-A.		
PD	22-MAR-1990.		
PF	06-SEP-1989; U03852.		
PR	06-SEP-1988; US-240624.		
PR	08-SEP-1988; US-241744.		
PR	13-SEP-1988; US-243739.		
PR	04-OCT-1988; US-253002.		
PR	19-JUN-1989; US-367641.		
PR	21-JUL-1989; US-382768.		
PA	(ITGE-) INT GENETIC ENG INC.		
PA	Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;		
DI	WPI; 90-115825/15.		
DR	P-PSDB; R09426.		
PT	Chimeric mouse-human antibodies - prep'd. using genes coding for		
PT	constant human region murine variable region, esp. to 3 tumour		
PS	antigen		
PS	Claim 13; Page 123 + Fig 29; 173pp; English.		
CC	Shown is the nucleotide sequence from the end of the oligo-dC tail		
CC	to the Jk1-Ck junction. The sequence is used in the prodn. of a		
CC	chimeric antibody mol. comprising two light chains and two heavy chains,		
CC	each having a constant region (human) and a variable region (murine)		
CC	having specificity to an antigen bound by murine monoclonal antibody		
CC	(WAB) ME4. The chimeric antibodies can be used for any purpose for		
CC	which the original murine MAbs can be used, with the advantage that		
CC	they are more compatible with the human body. They are esp. used for		
CC	the diagnosis and treatment of cancer.		
SQ	Sequence 444 BP; 109 A; 122 C; 94 G; 119 T;		
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Best Local Similarity	94.7%; Pred. No. 1.82e-214;		
Matches	360; Conservative 0; Mismatches 20; Indels 0; Gaps 0;		

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Qy	61	GATATCCAGATGACACAGACTACATCCTCCCTGCTCTGCTCTCTGGGACAGAGATCACC	120	
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Qy	121	ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA	180	
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Qy	181	GATGMACTATTAAACTCCTGATCTACTACATCAGATTACACTCAGGATCCCATCA	240	
Db	301	aggttcagtgccagtgggctcggagacagattattctctcaccattagcaacctggagcaa	360	
Qy	241	AGTTTCAGTGGCAGTGGGCTCGAACAAGATTATTTCTTCACATTATAAACCTGGAGCAA	300	
Db	361	gaagattttgccactctcttttggcaacagaggaataatactctcggacgttcggtgga	420	
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Db	421	ggcaccacaactgggaatcaa	440
Qy	361	GGGACCAAGCTGGAAATAA	380

RESULT 6			
ID	Q30759	standard; cDNA; 381 BP.	
AC	Q30759;		
DT	30-MAR-1993	(first entry)	
DE	p146-k3.		
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;		
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;		
KW	plasmid; p146k3; p146-h1; ss.		
OS	Synthetic.		
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FT	mat_peptide	61..381	
FT	/*tag= b		
PN	W09219759-A.		
PD	12-NOV-1992.		
PF	24-APR-1992; J00544.		
PF	25-APR-1991; JP-095476.		
PR	19-FEB-1992; JP-032084.		
PA	(CHUS ) CHUGAI SEIYAKU KK.		
PI	Bendig MW, Jones ST, Saldanha JW, Sato K, Tsuchiya M;		
DR	WPI; 92-398882/48.		
DR	P-PSDB; R29010.		
PT	Reconstituted human antibody to human interleukin-6 receptor -		
PT	has low antigenicity and contains mouse V-region complementarity		
PT	determining regions		
PS	Disclosure; Page 127-128; 207pp; Japanese.		
CC	The sequences given in Q30759 and Q31337 were used in example to		
CC	illustrate the production of a human antibody which recognises human		
CC	interleukin-6 receptor (IL-6R). The antibody comprises light (L)		
CC	chain and heavy (H) chain variable regions which were derived from a		
CC	mouse monoclonal antibody produced from the hybridoma AUK146-15 which		
CC	contained the plasmids p146-k3 and p146-h1.		
SQ	Sequence 381 BP; 106 A; 90 C; 86 G; 99 T;		

Query Match	87.7%;	Score 334;	DB 5;	Length 381;
Best Local Similarity	93.9%;	Pred. No. 2,98e-210;		
Matches 357;	Conservative	0;	Mismatches 23;	Indels 0;
Gaps	0;			
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Qy	1	ATGGTGTCTCAGTCAGTCTCTTGCTCTCTGCTCTGCTTTTCAGGTACCGAGTGT	60	
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Qy	61	GATATCCAGATGACACAGACTACATCTCTCTGTCTGCCTCTCTCGGAGACAGAGTCCACC	120	
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Qy	121	ATCAGTTGCGGGGCAAGTCAGGACATTAGCAGCTATTATTAACCTGGTATCAGCAAGAACCA	180	
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Qy	181	GATGGAACTATTAAACTCTGTACTACTACATCAAGATTACTCAGAGGTCCCATCA	240	
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Db	301	gaagatatgccagttactatttgcacacagggtatatacacttcogtggacgtttcgtgga	360
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Db	361	ggcaccagaattggaaatacaa	380
Qy	361	GGCACCAGCTGGAAATAAA	380

## RESULT 7

ID	Q56067	standard; cDNA to mRNA; 372 BP.
AC	Q56067;	
DC	09-AUG-1994	(first entry)
DE	Human IL-1 chimeric antibody CH cDNA.	
KE	Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;	
KW	light; L; chain; constant; region; variable; mouse; anti-human;	
KW	graft; CDR; complementarity determining region; heavy; H;	
KW	inflammatory disease; arteriosclerosis; detection;	
KW	diffused intravascular coagulation; leukemia; ss.	
OS	Synthetic.	
EH	Key	Location/Qualifiers
FT	sig_peptide	1..93
FT	/*tag= a	
FT	mat_peptide	94..372
FT	/*tag= b	
FT	WO9402627-A.	
PN	03-FEB-1994.	
PD	PN	
PF	08-JUL-1993; J00941.	
PR	16-JUL-1992; JP-189248.	
PR	(SAKA ) OTSUKA PHARM CO LTD.	
PI	Hirai Y, Nishida T, Omoto Y, Owens RJ;	
PI	WFI; 94-048885/06.	
DR	P-PSDB; R47206.	
PT	Mouse/human chimeric antibody against human interleukin-1 - for	
PT	treatment of diseases in which production of interleukin-1 is	
PT	abnormal, and for diagnostic imaging of interleukin-1 production	
PT	sites in vivo	
PS	Claim 1; Page 31-32; 58pp; Japanese.	
CC	The sequences given in Q56066-69 are the coding sequences for the	
CC	light and heavy chain, variable and constant regions of a chimeric	
CC	recombinant antibody against human interleukin-1 (IL-1). The antibody	
CC	has a light (L) chain in which the constant region is that of a human	
CC	antibody and the variable region is from a mouse anti-human IL-1	
CC	antibody or is a mouse-human graft containing the CDR regions of mouse	
CC	anti-human IL-1 antibody, and a heavy (H) chain in which the constant	
CC	region is that of a human antibody and the variable region is from a	
CC	mouse anti-human IL-1 antibody or is a mouse-human graft containing	
CC	the CDR regions of mouse anti-human IL-1 antibody, . The chimeric	
CC	antibody is used to treat diseases in which abnormal amounts of IL-1	
CC	are produced, eg. inflammatory disease, arteriosclerosis, diffused	
CC	intravascular coagulation or leukemia. It can also be labelled and	
CC	used for diagnostic imaging of IL-1 producing sites in vivo.	
SQ	Sequence	372 BP; 105 A; 93 C; 78 G; 96 T;

Query Match	84.8%;	Score 323;	DB 10;	Length 372;
Best Local Similarity	93.5%;	Pred. No. 1.57e-202;		
Matches 347;	Conservative 0;	Mismatches 24;	Indels 0;	Gaps 0;
<hr/>				
Db	1	tctgctcagttcccttggtctctgttgcctgtttccaaggaccacagtgtgatccag	60	
Qy	10	TCAGCTCAGTTCCCTTGSTCTGCTCTGCTCTCTTTTCAAGTACCAGATGTGATCCAG	69	
<hr/>				
Db	61	atgacacagactacatcctcctgtctgctctctctgggagacagagtcacatcaattgc	120	

Qy	70	ATGACACAGACTACATCCCTCCTCTGCTCCTCTGCTGGGACACAGAGTCACCAATCAGTTGC	129
Db	121	aggcaagtcagacattacaataatttaaacctggtticaacagaaacacagatggaact	180
Qy	130	AGGGCAAGCTCAGGACATTAGCAGGTTATTTAAACTGCTATCAGCAGNAACCGATGGAAC	189
Db	181	gttaaacctcgtatctacacatcaagattacaactcaggagtcctccatcaaggttcagt	240
Qy	190	ATTAACCTCTGATCTACTACATCAAGATTACATCAGGAGTCCCATCAAGGTTCAAT	249
Db	241	ggcagtggtgctggaacagattattctcaccattagcaaacctggagaagaagatgct	300
Qy	250	GGCAGTGGGCTCGACACATTATTTCTCTCCACTTTAAACAACCTGGAGCAAGACACATT	309
Db	301	gccacttactcttgccaacacagggtaaaacccctccgtggagcttcggtggagggaccaag	360
Qy	310	GCCACTTACTTTTGGCAACAGGGTTAACGCTTCGCTACACGTTCCGAGGGGGGACCAAG	369
Db	361	ctgggaattcaa	371
Qy	370	CTGCAAAATAAA	380

## RESULT

ID	Q12017 standard; DNA; 402 BP.
AC	Q12017;
DT	19-AUG-1991 (first entry)
DE	Sequence encoding mouse Mab 1C11 L chain V region.
KW	HIV-1; chimera; ds.
OS	Mus sp.
FH	Key
FT	Location/Qualifiers
CD5	22..402
FT	/*tag= a
PN	W09107494-A.
PD	PD 30-MAY-1991.
PF	13-NOV-1990; U06627.
PR	13-NOV-1989; US-433703.
PA	(XOMA-) Xoma Corp.
PI	Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
DR	WPI; 91-178106/24.
DR	P-PSDB; R12237.
PT	New chimeric mouse human antibodies - used in treatment, diagnosis
PT	and prophylaxis of HIV infections.
PS	Disclosure; Fig 13; 108pp; English.
CC	The mouse VL gene product may be used to produce chimeric mouse-
CC	human Abs against HIV-1 comprising human Ig constant regions and
CC	murine variable regions. These novel sequences are useful in
CC	treatment, diagnosis and prophylaxis of HIV infections, and may be
CC	produced by a bacterial, yeast or mammalian expression system.
SO	Sequence 402 BP; 108 A; 99 C; 88 G; 107 T;

	Query Match	84.5%;	Score 322;	DB 2;	Length 402;
	Best Local Similarity	92.4%;	Pred. No. 7.88e-202;		
	Matches 351;	Conservative 0;	Mismatches 29;	Indels 0;	Gaps 0;
Db	22	atggtctctctgctcagttctctctggtctctctgttttcaagggtaccagatgt	81		
Qy	1	ATGGTGTCTCAGCTCAGTTCCTGGTCTGCTGTCTGTTTTCAAGGTACCAGATGT	60		
Db	82	gatatcaagatgacacagactacatcctcctgtctgtcctctctctgtgggacagatcacc	141		
Qy	61	CATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCCTCTCTGGGACAGACAGTCACT	120		
Db	142	atcagttgcadgtcgaagctcagggcattacgaattatttaaacctggtatctcacgagaacca	201		



Db	25	atgatgctctgctcagttctcttgggtctcctgttgctctgtttcaaggtaccagatgt	84
Qy	1	ATGGTGTCTTCAGCTCAGTTCCTTGGCTCTCTGTGCTCTGTGTTTCAAGGTACCAGATGT	60
Db	85	gataccagatgacacagactgcatcctcctgtgcctctctcgggagacagagtcaac	144
Qy	51	GATATCCAGATGACAGACTACATCTCTCTGTCTGCTCTCTGGGAGACAGACTCACC	120
Db	145	atcagttgcagtgcaagtcagagcattagtaattatttaaactggtatcaacagaatacca	204
Qy	121	ATCAGTTGCAGCGGCACTACGACATTTACAGCTATTTTAACTGGTATCAGCAGAAACCA	180
Db	205	gatggaactgttaaactcctgatcttttactcataaattacactcgggagtcctcatca	264
Qy	181	GATGGAACTATTAAACTCTCTGATCTACTACATCAAGATTACTCAGAGGTCCCATCA	240
Db	265	aggttcagttgcaggtgggtccgggacagattatctctcaccatcagcaacctggagcct	324
Qy	241	AGGTTCACTGGCAGTGGGTCTGGAAACAGATTATCTCTACCATTTAAACACCTTGGAGCA	300
Db	325	gaagatatggccatttaactttgttcacagtatagtaagcttcogtggacgtttcogtggga	384
Qy	301	GAAGACATTGGCACTTACTTTTGGCCACAGGGTAAACAGCTTCOGTACAGCTTCGGAGGG	360
Db	385	ggcaccagagctggaatacaa	404
Qy	361	GGGACCAAGCTGGAAATAAA	380

RESULT	11
ID	Q45438 standard; cDNA to mRNA; 408 BP.
AC	Q45438;
DT	18-NOV-1994 (first entry)
DE	KM641 H chain variable region.
DE	Monoclonal antibody; Ab; ganglioside GM2; chimera;
KW	chimeric antibody; expression vector; heavy; light; chain;
KW	hypervariable region; CDR; constant region; hybridoma;
KW	Ig; immunoglobulin; promoter; enhancer; ds.
OS	Mus musculus.
FT	Key Location/Qualifiers
FT	CDS 5..408
FT	/*tag= a
FT	/note= "excluding stop codon"
FT	sig_peptide 5..84
FT	/*tag= b
PN	AU9346181-A.
PD	17-MAR-1994.
PF	07-SEP-1993; 046181.
PR	07-SEP-1992; JP-238452.
PI	(KYOW ) KYOWA HAKKO KOGYO KK.
PI	Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
PI	Shitara K;
DR	WPI; 94-126857/16.
DR	P-PSDB; R53340.
PT	Humanised antibody specific for ganglioside GM2 - used for
PT	producing a cytotoxic effect on cancers such as melanoma,
PT	neuroblastoma and glioma.
PS	Reference example 2; Page 115-116; 191pp; English.
CC	Example 2 describes the construction of the vector pCh1641HA1
CC	for chimeric human antibody H chain expression.
CC	mRNA from mouse anti-CD3 monoclonal Ab KM641-producing cells
CC	was isolated and KM641 H and L chain cDNAs isolated.
CC	The base sequences of the Ig variable regions in KM641

	CC	H chain cDNA (pKM641H)3 and KM641 L chain cDNA (pKM641L)A2)			
	CC	are given in Q45438-39. A KM641-derived chimeric human			
	CC	Ab H chain expression vector was constructed by joining			
	CC	the H chain variable region gene from pKM641H)3 to a			
	CC	vector for chimeric human Ab H chain expression using			
	CC	the synthetic DNAs given in Q63439 and Q63440.			
	SQ	Sequence 408 BP; 102 A; 102 C; 94 G; 110 T;			
		Query Match 79.8%; Score 304; DB 11; Length 408;			
		Best Local Similarity 90.0%; Pred. No. 3,286-189;			
		Matches 342; Conservative 0; Mismatches 38; Indels 0; Gaps 0;			
Df	25	atgatgtcctctgctcaagttcccttgcttgcctgttgttcctgaaggaccagtgt 84       			
Qy	1	ATGGTGCTCAGCTCAAGTTCCTCGGTGCTGCTTTTCAAGGTACCATGACT 60 			
Df	85	gataccagattcacacagactcatccctcgctgctctctggagacagatgcc 144       			
Qy	61	GNTATCCAGTACACAGACTACATCCTCCTCTCTGCCCTCTGGGCAGACAGATGCC 120 			
Df	145	atcagtttgtagtccaagtgcaggacattagtaattttaaatcgggtatcaacagaaca 204 			
Qy	121	ATCAGTTGACGGCGAACTCAGGACATTAGCAGATTATTTTAACATGGTATTACGACAACCA 180 			
Df	205	gatggaacctgttaaactcctgatcttattactcataaaattcaactcggagtcacca 264       			
Qy	181	GATGGGAATAATTAAACTCCTGGATCTACTCACATCATAGAATTACACTCAGGAGTCCCCATCA 240 			
Df	265	aagtttcagtgccggtgggtccgggacagattctctccaccatcagaacactggagcct 324 			
Qy	241	AGGTTTCAGTGGCAGTGGGTCTGSAAACAGATTATTTCTCACCATTAAACAACCTGGAGCAA 300 			
Df	325	ggagatatigccaacttacttttgtcatcagtatagtaagtttcogtggagctcgggtgga 384       			
Qy	301	GAAAGACATTTGCCACTTACTTTTTGGCAACGGGTACACGGCTCCGTACACGTTCGAGGG 360 			
Df	385	ggcaccgaagctggaaaatcaa 404 			
Qy	361	GGGACCAGCTGCAAAAATAAA 380 			

RESULT 12

ID T05313 standard; DNA; 324 BP.

AC T05313;

DT 02-FEB-1996 (first entry)

DE B-cell lymphoma CH12 IgM light chain DNA.

KW Monoclonal antibody; WAB; SCH94.03; hybridoma; central nervous system;

KW CNS; demyelination; multiple sclerosis; neural disease; therapeutic;

KW B-cell lymphoma; CH12; IgM; ds.

OS Mus sp.

PN W09530004-A1.

PD 09-NOV-1995.

PF 27-APR-1995; U05262.

PR 29-APR-1994; US-236520.

PA (MAYO-) MAYO FOUNDATION.

PI Miller DJ, Rodriguez M;

PR WP1; 95-393077/50.

DT Monoclonal antibodies which stimulate central nervous system

PT re-myelination - are produced by hybridoma ATCC CRL 11677, for

PT treating multiple sclerosis, and viral or post-neural diseases of

PT the CNS.

PS Disclosure; Page 37; 63pp; English.

CC The light and heavy chain variable region gene sequences (given

CC in T05311-12, respectively) of monoclonal antibody SCH94.03



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CC showed extensive sequence similarity with corresp. sequences  
 CC (705313-14) of the IgM produced by B-cell lymphoma CH12.  
 SQ Sequence 324 BP; 96 A; 81 C; 71 G; 76 T; 76 T;  
 Query Match 77.2%; Score 294; DB 16; Length 324;  
 Best Local Similarity 95.9%; Pred. No. 3.30e-182;  
 Matches 307; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 Db 1 gatatccagatgacacagactacatcctcctgtctgtcctctctctgtgggagacagatcacc 60  
 Qy 61 GATATCCAGATGACACAGACTACATCTCCCTCTGTCTGTGGGAGACAGTCAACC 120  
 Db 61 atcagttcgaggcgcaagtcaggacattagcaattatttaaacctgtgtatcagcagaaccca 120  
 Qy 121 ATCAGTTGCGAGGCGCAAGTCAGGACATATAGCAGTTATTTAAACCTGGTATCAGCGAAACCA 180  
 Db 121 gatgaactgttaaacctcctgatctactacatcaagattacactcaggagtcacatca 180  
 Qy 181 GATGGAATTAATAACTCTCATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240  
 Db 181 aggttcagtcgagtcgggtcggaacagattattctccaccattagcaacctggagca 240  
 Qy 241 AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATCTCTCACCATTAAACACCTGGAGCA 300  
 Db 241 gaagattatgccacttatttggcaacagggttaatacagttctcctcagtcgtcggtgga 300  
 Qy 301 GAAGACATTGCCACTTACTTTTGGCAACAGGTTACACGGTCCGTACACGTTCCGAGGG 360  
 Db 301 ggcaccaagctggaataca 320  
 Qy 361 GGGACCAAGCTGGAAATAA 380  
 RESULT 13  
 ID Q81076 standard; cDNA; 913 BP.  
 AC Q81076;  
 DT 14-MAR-1995 (first entry)  
 DE Bispecific CD3-L6FvIg antibody derivative coding sequence.  
 KW fusion protein; recombinant bispecific single chain antibody;  
 KW helical peptide linker; anti-L6 antibody; tumour cell antigen;  
 KW anti-CD3 antibody; variable region; ss.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 7..75  
 FT /\*tag= a  
 FT /\*note= "L6 light chain variable region leader"  
 FT CDS 7..912  
 FT /\*tag= b  
 FT misc RNA 76..819  
 FT /\*tag= c  
 FT /\*note= "encodes CD3 VL-VH fusion"  
 FT misc RNA 820..828  
 FT /\*tag= d  
 FT /\*note= "encodes hinge region of Fc domain"  
 FT misc RNA 829..912  
 FT /\*tag= e  
 FT /\*note= "encodes helical peptide linker"  
 PN EP-61046-A.  
 PD 10-AUG-1994.  
 PE 31-JAN-1994; 300692.  
 PR 01-FEB-1993; US-013420.  
 PR 13-SEP-1993; US-121054.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PI Bajorath J, Fell PH, Gilliland IK, Hayden MS, Ledbetter JA;

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PI Lineley PS;  
 DR WPI; 94-250885/31.  
 DR P-PSDB; R60206.  
 PT Expression vector encoding bispecific fusion protein - having  
 PT binding domains for separate targets joined by helical peptide,  
 PT useful e.g. for diagnosis and treatment  
 PS Example 1; Fig 11; 50pp; English.  
 CC The VL and VH sequences of the anti-CD3 hybridoma G19-4 were  
 CC amplified by PCR methods. A gene fusion was constructed from the  
 CC two amplified domains and a (Gly4Ser)3 linker. The amino  
 CC terminus of the VL-VH fusion cassette was fused at the SalI site to  
 CC the L6 light chain variable region leader peptide and the  
 CC carboxy-terminus was fused directly to the hinge region of the Fc  
 CC domain at the BclI site and/or to a short "helical" peptide linker  
 CC to construct the bispecific CD3-L6FvIg antibody derivative. The  
 CC variable regions for L6 were fused in frame to the opposite end of  
 CC the helical linker (not included in Q81076).  
 SQ Sequence 913 BP; 252 A; 223 C; 228 G; 210 T;  
 Query Match 73.5%; Score 280; DB 12; Length 913;  
 Best Local Similarity 94.3%; Pred. No. 2.05e-172;  
 Matches 298; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
 Db 76 gacatccagatgacacagactacatcctcctgtctgtcctctctgtgggagacagatcacc 135  
 Qy 61 GATATCCAGATGACACAGACTACATCTCCCTCTGTCTGTGGGAGACAGTCAACC 120  
 Db 136 atcagttcgaggcgcaagtcaggacattcgcattattttaaactgtgtatcagcagaaccca 195  
 Qy 121 ATCAGTTGCGAGGCGCAAGTCAGGACATTTAGCAGTTATTTAACTGGTATCAGCGAAACCA 180  
 Db 196 gatggaactgttaaacctcctgatctactacatcaagattacactcaggagtcacatca 255  
 Qy 181 GATGGAATTAATAACTCTCATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240  
 Db 256 aggttcagtcgagtcgggtcggaacagattattctcaccattgccaacctgcaacca 315  
 Qy 241 AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTTCTCTCACCATTAAACACCTGGAGCAA 300  
 Db 316 gaagattatgccacttactttggcaacagggttaatacagttcctcgtggagtcgtgga 375  
 Qy 301 GAAGACATTGCCACTTACTTTTGGCAACAGGGTAAACACGCTTCGTTACGTTCCGAGGG 360  
 Db 376 ggcaccaaacctggttaa 391  
 Qy 361 GGGACCAAGCTGGAAA 376  
 RESULT 14  
 ID Q62957 standard; DNA; 831 BP.  
 AC Q62957;  
 DT 09-SEP-1994 (first entry)  
 DE Anti-influenza N10 scFv.  
 KW Monoclonal antibody N10; target binding polypeptide; scFv;  
 KW scFv; single chain antibody; protein secretion; FLAG;  
 KW Escherichia coli; antibody engineering; humanized antibody;  
 KW influenza virus; neuraminidase; ss.  
 OS Not specified.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..66  
 FT /\*tag= a  
 FT /\*note= "pelB signal sequence"  
 PN W09407921-A.  
 PD 14-APR-1994.

PR	28-MAY-1993; US-070160.
PA	(SCRI ) SCRIPPS RES INST.
PI	Leturcq DJ, Mathison JC, Moriarty AM, Tobias PS;
PI	Ulevitch RJ;
DR	WPI; 95-022719/03.
DR	P-PSDB; R64204.
PT	Hybridoma cell lines produce MAb which inhibit CD14-mediated cell activation - for detecting CD14 in a sample and to inhibit the binding of LPS to CD14.
PT	Disclosure; Fig 5; 91pp; English.
CC	Anti-human soluble CD14 receptor MAB 18E12 may be used to detect CD14 in cell samples, to inhibit binding of LPS to CD14 or a LPS/CD14 complex to a cell, to inhibit CD14-mediated activation of a cell expressing CD14 receptor, and for sepsis therapy.
SQ	Sequence    627 BP;    184 A;    161 G;    139 T;
	Query Match                  64.0%;    Score 244;    DB 13;    Length 627;
	Best Local Similarity    91.6%;    Pred. No. 2.68e-147;
	Matches    285;    Conservative         0;    Mismatches    23;    Indels      3;    Gaps        1;

Db  
1 atgacccagactcattccctgtctgcctctctgggagacagagtaccatcagttgc 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy  
70 ATGACACAGACTTCACTCCTCCCTGTCTGCCCTCTCTGGGACACAGAGTCACCATTGTC 129

Db	61	aggcgcaagtccaggacattaaagaattattttaaacctggatctcaacgaggagccaaagtggaact	120
Qy	130	AGGCGCAAGTCAGGACATTAGCAGCTATTTTAAACTGGTATTCAGCAGCAAAACGAGATGGAAC	189
Db	121	gttaaggtccactactactacacatcaagattacaactccaggaggtcccatccaaggttcagt	180
Qy	190	ATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCAAGGTTTCAGT	249
Db	181	ggcagtggggtctggacaagattattctctcaacattagacaacctggagacaagaagaatttt	240
Qy	250	GGCAGTGGGCTGGACAAGATTATTCCTCACCAATTAAACAACCTGGAGCAAGAAGACATT	309
Db	241	gccacttaactt----caacgggggtgatacagttccgtggacacttcggtggagggacacaag	297
Qy	310	GCCACTTACTTTTCCCAACAGGGGTAAACGGCTTCGCTACACGCTTCGGAGGGGGGCCAAG	369
Db	298	ctggaaatcaa	308
Qy	370	CTGGAATATAA	380

Search completed: Mon Jul 8 08:53:37 1996  
Job time : 40 secs.

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WATERMAN

(TM)

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MPsrch\_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:53:55 1996; MacPar time 178.28 Seconds

Tabular output not generated.  
768.287 Million cell updates/sec

Title: >US-08-137-117B-28

Description: (1-381) from US08137117B.seq

Perfect Score: 381

N.A. Sequence: 1 ATGGTGTCTCAGTCAGCTT.....GGACCAAGTCGGAATAAAT 381

Comp: TACACAGAGTCAGTCA.....CCTGGTCGACCTTTATTTA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-STS

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56  
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62  
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80  
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86  
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92  
93:EST93 94:EST94  
EST-STS-TWO

Database:

95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5  
100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10  
105:gnEST11 106:gnEST12 107:gnEST13 108:gnEST14 109:gnEST15  
110:gnEST16 111:gnEST17 112:gnEST18 113:gnEST19 114:gnEST20  
115:gnEST21 116:gnEST22 117:gnEST23 118:gnEST24 119:gnEST25  
120:gnEST26 121:gnEST27 122:gnEST28 123:gnEST29  
124:gnEST30 125:gnEST31 126:gnEST32 127:gnEST33

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

Statistics: Mean 10.019; Variance 1.775; scale 5.646

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	178	46.7	393	69	T27593	EST100653 Homo sapien	0.00e+00
2	178	46.7	393	127	HST27593	EST100653 Homo sapien	0.00e+00
3	176	46.2	516	52	R67559	y142h11.r1 Homo sapie	0.00e+00
4	165	43.3	395	114	HS11211	EST69384 Homo sapiens	0.00e+00
5	165	43.3	395	70	T29112	EST69384 Homo sapiens	0.00e+00
6	146	38.3	288	69	T27581	EST100107 Homo sapien	9.92e-265
7	146	38.3	288	127	HST27581	EST100107 Homo sapien	9.92e-265
8	138	36.2	288	69	T27721	EST13641 Homo sapiens	1.80e-246
9	138	36.2	288	127	HST27721	EST13641 Homo sapiens	1.80e-246
10	124	32.5	451	42	R31204	yh62a07.r1 Homo sapie	1.01e-214
11	120	31.5	335	47	R49881	yj55f09.r1 Homo sapie	1.05e-205
12	115	30.2	243	11	H25952	y156a07.r1 Homo sapie	1.81e-194
13	108	28.3	503	41	R28232	yh57e08.r1 Homo sapie	8.10e-179
14	107	28.1	463	53	R69532	y182d09.r1 Homo sapie	1.37e-176
15	100	26.2	332	118	HS34210	EST77181 Homo sapiens	4.69e-161
16	100	26.2	332	70	T29342	EST77181 Homo sapiens	4.69e-161
17	93	24.4	279	122	HS65610	EST89211 Homo sapiens	1.22e-145
18	93	24.4	279	70	T29656	EST89211 Homo sapiens	1.22e-145
19	90	23.6	451	86	T90236	ye15d10.r1 Homo sapie	4.50e-139
20	85	22.3	434	87	T93178	ye24e07.r1 Homo sapie	3.45e-128
21	84	22.0	210	53	R69482	yj83c03.r1 Homo sapie	5.06e-126
22	82	21.5	360	56	R79907	y185f01.r1 Homo sapie	1.07e-121
23	79	20.7	383	70	T29916	EST99871 Homo sapiens	3.07e-115
24	79	20.7	383	125	HS91615	EST99871 Homo sapiens	3.07e-115
25	78	20.5	397	47	R49771	yj55c03.r1 Homo sapie	4.29e-113
26	77	20.2	261	46	R46878	yj54h03.r1 Homo sapie	5.94e-111
27	76	19.9	381	114	HS11411	EST69430 Homo sapiens	8.15e-109
28	76	19.9	381	70	T29114	EST69430 Homo sapiens	8.15e-109
29	72	18.9	166	11	H25744	y150a11.r1 Homo sapie	2.62e-100
30	71	18.6	385	11	H26475	y151g05.r1 Homo sapie	3.42e-98
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32	69	18.1	390	17	H45841	yp22b04.r1 Homo sapie	5.63e-94
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34	68	17.8	438	51	R46493	y122f09.r1 Homo sapie	7.10e-92
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39	64	16.8	387	53	R70292	yj81e03.r1 Homo sapie	1.59e-83
40	63	16.5	123	115	HS154207	yq66g05.r1 Homo sapie	1.88e-81
41	63	16.5	123	61	R98154	yq66g05.r1 Homo sapie	1.88e-81
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## ALIGNMENTS

RESULT	1	T27593	393 bp	mRNA	EST	06-SEP-1995
LOCUS						

**DEFINITION** EST100653 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region (GB:L01279) (HT:3043).

ACCESSION	T27593
KEYWORDS	EST.
SOURCE	human primer-M13 Reverse library=Human Pancreas.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chondata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 393)

1 (bases 1 to 393)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.C., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Springs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.-L., Kunsch, C., Ji, H., Li, H., Weissner, P., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.C. and Venter, J.J.

**TITLE** Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence Unpublished (1995)

**JOURNAL**

COMMENT

Other\_ESTs: THC24356  
Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: tdbinfo@tdb.tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please contact the TIGR Database  
(tdbinfo@tdb.tigr.org).

NCBI gi: 609691	
Location/Qualifiers	
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/note="human"	
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ORIGIN	2 others

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Matches 272; Conservative 0; Mismatches 90; Indels 1; Gaps 1;

Db 5 ggtcagctctggggtctctgctaactcggtccgcagggtgccagatgtgacatccagatg 64  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 13 GCTCAGTTCCTGGTCCCTGTTGCTCTCTTTCAAGGTACAGATGCTGATATCCAGATG 72

[illegible]

Db 125 qcaagtcaagacattatgcacctttttaattggtatcagcagaaccagggacagccct 184

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Qy	193	AACCTCTGTATCTACTACACATCAAGATTCACTCAGGAGTCCCATCAAGGTTCAGTGGC	252
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Qy	253	AGTGGGCTGGACAGATTATCTCTCACCATTAAACAACCTGGAGGAAGACAGACTTGCC	312
Db	305	acttactactgtcaacagagttncaettatgnctcggacggttggccaaagggaaccaaggt	364
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RESULT 2  
ID HST27593 standard: RNA; EST: 393 BP.

AC T27593;  
 DT 12-JAN-1995 (Rel. 42, Created)  
 DT 07-SEP-1995 (Rel. 45, Last updated, Version 2)  
 DE ESF100653 Homo sapiens cDNA 5' end similar to immunoglobulin kappa  
 DE light chain, v region (GB:L01279) (HT:3043).  
 KW EST.

OS Homo sapiens (human)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea;  
RN [1]

1-393  
 Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,  
 Bult C.J., Lee N., Kirkness E.F., Weinstein K.G., Gocayne J.D.,  
 White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,  
 Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,  
 FitzGerald L.M., FitzHugh W.M., Frichman J.L., Geohagen N.S.M.,  
 Glodex A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,  
 Kelley J.M., Klimesk K.M., Kelley J.C., Liu L.I., Marmaros S.M.,  
 Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,  
 Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,  
 Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,  
 Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,  
 Coleman T.A., Collins E.J., Dimke D., Feng P., Ferlie A.,  
 Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,  
 Gruber J., Hudson P., Kim A., Korzak D.L., Kunsch C., Ji H., Li H.,  
 Meisner P.S., Olsen H., Raymond L., Wei Y.F., Wang J., Xu C.,  
 Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,  
 Haehtline W.A., Fields C., Frazer C.M., Venter J.C.:  
 "Initial Assessment of Human Gene Diversity and Expression  
 Patterns Based Upon 52 Million Basepairs of cDNA Sequence";  
 Unpublished. RL

CC Other\_ESTs: THC24356 Contact: Venter, JC The Institute for Genomic  
CC Research 323 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056  
CC CC Fax: 3018699423 Email: tdbinfo@db.tigr.org For clone availability,  
CC additional sequence and expression information related to this EST,  
CC please contact the TIGR database (tdbinfo@db.tigr.org). NCBI gi:  
CC 609691

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# III









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ADAMS, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., FitzHugh, M.M., Fritchman, J.L., Geodhagen, N.S.M., Glodek, A., Gnehm, J.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosch, C.A.,

OS Homo sapiens (human)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.  
[1]  
RP 1-288  
RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,  
RA Bult C.J., Lee N., Kirkness E.F., Weinstein K.G., Gocayne J.D.

(Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer=M13R1 Reitel=Not I Reite=Eco RI Female Placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' CTCTGAAGAATTCGGCGGCAGAGATTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaído.

*Homo sapiens*

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 451)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lemon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project  
Unpublished (1995)

Contact: Wilson RK  
WashU-Merck EST Project

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Contact: Wilson RK  
WashU-Merck EST Pro

Contact: Wilson RK  
WashU-Merck EST Project

High quality sequence stops: 218  
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

NCBI gi: 787047

NCBI gi: 787047

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l Similarity 82.6%; Pred. No. 1.01e-214;

161; Conservative 0; Mismatches 33; Indels 1; Gaps

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CACAGACTACATCCTCCCTGCTGCTCTCTGGGAGACAGAGTCACCATCAGTTCAGG 132

caagtcagaccattagcgactattaaattggtatcagcagaaaccagngaaagcccc 225

aaactnctgactca 240

||||| |||||  
||||| |||||

ATTACCI CIGI CIA 200

Jul 8 08:46

US-08-137-117B-28.rst

15

LOCUS R49881 335 bp mRNA EST 18-MAY-1995  
DEFINITION YJ55f09.r1 Homo sapiens cDNA clone 152681 5' similar to  
gb:X00965\_cds1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN); .  
ACCESSION R49881  
KEYWORDS EST.  
SOURCE human clone=152681 library=Soares breast 2NbHBst vector=pt7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=M13Rp1 Reitel=Not I Reite2=Eco RI Adult female.  
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-  
TGTACCAATCTCAAGTCGAGCGGCCGCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pt7T3 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 230. Library constructed by Bento  
Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 335)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 235  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 811783  
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source 1..335  
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ORIGIN

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Matches 195; Conservative 0; Mismatches 51; Indels 4; Gaps 4;

Db 23 gtcagctctcctggtcctgctactctggctccgagtgccagatgtgacatccagatg 82  
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Db 83 accagctctccatcttccctgtctgtctgttaggagacagatcaccatcacttgcgg 142  
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Jul 8 08:46

US-08-137-117B-28.rst

16

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Qy 192 TAAACTCTCTGATCTACTACATCAATACATCAGGAG-TCCCATCAAGG-TTCAGT 249  
Db 263 ggcagctggg 272  
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RESULT 12  
LOCUS H25952 243 bp mRNA EST 10-JUL-1995  
DEFINITION v15fa07.r1 Homo sapiens cDNA clone 162228 5' similar to  
gb:X00965\_cds1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN); .  
ACCESSION H25952  
KEYWORDS EST.  
SOURCE human clone=162228 library=Soares breast 3NbHBst vector=pt7T3D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin  
resistant) primer=M13Rp1 Reitel=Not I Reite2=Eco RI Adult human.  
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-  
TGTACCAATCTCAAGTCGAGCGGCCGCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),  
digested with Not I and cloned into the Not I and Eco RI sites of a  
modified pt7T3 vector (Pharmacia). Library went through one round  
of normalization to a Cot = 20. Library constructed by Bento Soares  
and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 243)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 895075  
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Query Match 30.2%; Score 115; DB 11; Length 243;  
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DT	09-JAN-1995 (Rel. 42, Created)	
DE	08-SEP-1995 (Rel. 45, Last updated, Version 2)	
DT	EST71181 Homo sapiens cDNA 5' end similar to immunoglobulin kappa	
DE	light chain, V region (GB:M29469) (HT:3066).	
KW	EST.	
OS	Homo sapiens (human)	
OC	Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;	
OC	Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.	
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RP	1-332	
RA	Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,	
RA	Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,	
RA	White O., Sutton G., Blake J.C., Brandon R.C., Chiu M.W.,	
RA	Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,	
RA	FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geophagen N.S.M.,	
RA	Glocke A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,	
RA	Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,	

Search completed: Mon Jul 8 08:57:00 1996  
Job time : 185 secs.

\*\*\*\*\*

WPS RELEASE  
(TM)

\*\*\*\*\*

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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WPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:57:18 1996; MasPar time 281.30 Seconds  
Tabular output not generated. 1034.412 Million cell updates/sec

Title: >US-08-137-117B-30

Description: (1-411) from US08137117B.seq

Perfect Score: 411

N.A. Sequence: 1 ATGAGAGTGGTGGATTCTTTT.....CCTCAGTCACGCTCTCTCA 411  
Comp: TACTCTCAGCTACTAGAAAA.....GGAGTCAGTGGCAGAGGT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 264399 seqs, 333985056 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-new1

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN  
9:PRI1 10:PRI2 11:PRI3 12:PRO1 13:PRO2 14:ROD 15:SYN  
16:UNC 17:VRT 18:VIR

Database: genbank91

19:BCT1 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7  
26:INV1 27:INV2 28:INV3 29:INV4 30:INV5 31:MAM1 32:MAM2  
33:PA1 34:PA2 35:PA3 36:PHG 37:PLN1 38:PLN2 39:PLN3  
40:PLN4 41:PLN5 42:PLN6 43:PLN7 44:PRI1 45:PRI2 46:PRI3  
47:PRI4 48:PRI5 49:PRI6 50:PRI7 51:PRI8 52:PRI9 53:ROD1  
54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD6 59:ROD7 60:STR  
61:SYN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5  
68:VRL6 69:VRT1 70:VRT2 71:VRT3

Database: genbank-new11

72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN  
79:PRI1 80:PRI2 81:PRI3 82:ROD 83:STR 84:SYN 85:UNA  
86:VRL 87:VRT

Database: u-emb144 91

88:part1

Statistics: Mean 10.250; Variance 3.740; scale 2.741

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	330	80.3	408 56	MUSIGHDOA	Mouse Ig rearranged H	0.00e+00
2	323	78.6	399 56	MUSIGHDOB	Mouse Ig rearranged H	0.00e+00
3	319	77.6	450 54	MMIGVHR2	Mouse mRNA for immuno	0.00e+00
4	314	76.4	417 54	MMU05284	Mus musculus BALB/c/J	0.00e+00
5	313	76.2	402 56	MUSIGHDOC	Mouse Ig rearranged H	0.00e+00
6	307	74.7	460 56	MUSIGHXX	Mouse Ig rearranged g	0.00e+00
7	297	72.3	485 56	MUSIGHAAC	Mouse Ig rearranged g	7.50e-298
8	289	70.3	358 57	MUSOHP138G	Mus musculus mRNA for	1.20e-288
9	284	69.1	358 57	MUSOHP7D7G	Mus musculus mRNA for	6.68e-283
10	284	69.1	434 56	MUSIGHNUL1	Mus musculus germline	6.68e-283
11	282	68.6	492 56	MUSIGHGCK	Mouse Ig rearranged m	1.33e-280
12	279	67.9	357 56	MUSIGLAM	Mouse IgM H-chain lam	3.70e-277
13	274	66.7	402 56	MUSIGHNOH	Mouse Ig active heavy	2.03e-271
14	272	66.2	470 56	MUSIGHXY	Mouse Ig rearranged g	4.00e-269
15	272	66.2	503 56	MUSIGHAAO	Mouse Ig rearranged g	4.00e-269
16	272	66.2	702 56	MUSIGG4014	Mus musculus rearrang	4.00e-269
17	271	65.9	351 56	MUSIGHJY	Mouse Ig active heavy	5.62e-268
18	271	65.9	358 57	MUSOHP57G	Mus musculus mRNA for	5.62e-268
19	268	65.2	348 54	MMRNA246	M.musculus (BALB/c) I	1.55e-264
20	265	64.5	342 56	MUSIGHAAG	Mouse Ig rearranged h	4.25e-261
21	263	64.0	348 56	MUSIGHACW	Mouse Ig H-chain mRNA	8.33e-259
22	262	63.7	358 57	MUSOHP19G	Mus musculus mRNA for	1.17e-257
23	259	63.0	502 56	MUSIGHNUL	Mus musculus rearrang	3.18e-254
24	257	62.5	439 56	MUSIGHDS	Mouse Ig active mu-ch	6.20e-252
25	256	62.3	417 14	MM16690	Mus musculus Ig heavy	8.64e-251
26	256	62.3	417 82	MMU16690	Mus musculus Ig heavy	8.64e-251
27	255	62.0	484 53	MMIGAM32	Mouse rearranged V(H)	1.21e-249
28	254	61.8	342 56	MUSIGHZ2	Mouse IgG-2a anti-p-a	1.68e-248
29	254	61.8	826 61	XXU05272	Synthetic construct c	1.68e-248
30	252	61.3	342 59	S54194	immunoglobulin heavy	3.26e-246
31	248	60.3	339 55	MMU25121	Mus musculus anti-eta	1.22e-241
32	248	60.3	408 56	MUSIGHCA	Mouse Ig family 36-60	1.22e-241
33	246	59.9	342 56	MUSIGHAAA	Mouse IgG-1 anti-p-az	2.36e-239
34	243	59.1	351 54	MMU15297	Mus musculus immunogl	6.31e-236
35	242	58.9	358 59	S74721	Ig VH-anti-human tran	8.75e-235
36	241	58.6	405 14	MMU16687	Mus musculus Ig heavy	1.21e-233
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38	240	58.4	288 59	S77976	Ig Vgam3.2-anti-human	1.68e-232
39	240	58.4	318 53	MMIGH11	M.musculus mRNA (L20-	1.68e-232
40	240	58.4	336 56	MUSIGHZK	Mouse IgG-1 anti-p-az	1.68e-232
41	239	58.2	294 56	MUSIGHAAX	Mouse Ig gamma-chain	2.33e-231
42	238	57.9	318 56	MUSIGHB29	Mouse IgG-1 anti-p-az	3.22e-230
43	238	57.9	354 55	MMVHMRB9	M.musculus mRNA for I	3.22e-230
44	237	57.7	340 54	MMRNA1VHC	M.musculus mRNA for i	4.45e-229
45	237	57.7	428 56	MUSIGME7A	Mus musculus monoclon	4.45e-229

## ALIGNMENTS

RESULT 1  
LOCUS MUSIGHDOA 408 bp mRNA ROD 28-APR-1995  
DEFINITION Mouse Ig rearranged H-chain mRNA V-region, 5' end of cds.  
ACCESSION L20961  
KEYWORDS V-region; anti-HLA antibody; antibody;  
immunoglobulin heavy chain; monoclonal antibody; processed gene.  
SOURCE Mus musculus (strain BALB/c, sub species domesticus) male adult  
hyperimmunized spleen cDNA to mRNA.  
ORGANISM Mus musculus

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US-08-137-117B-30.rge

3

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 408)  
AUTHORS Iwasaki, Y., Takabatake, H., Shinji, T., Monestier, M. and Ferrone, S.  
TITLE Structural profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic system

JOURNAL Eur. J. Immunol. 24 (11), 2874-2881 (1994)

MEDLINE 95045941

COMMENT NCBI gi: 309344

FEATURES Location/Qualifiers

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349..367  
368..408

exon

CDS

BASE COUNT 99 a 109 c 92 g 108 t

ORIGIN

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Best Local Similarity 92.0%; Pred. No. 0.00e+00;  
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

Db 1 atgagatgctgattcttttggctgttcacagccttctcgtggtatcctgtcgtatg 60  
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Qy 1 ATGAGAGTGTGATTCTTTTGGCTGTTCCAGCCTTTCTCGTATCCTGTCGATGC 60

exon

exon

exon

BASE COUNT 99 a 109 c 92 g 108 t

ORIGIN

Query Match 80.3%; Score 330; DB 56; Length 408;  
Best Local Similarity 92.0%; Pred. No. 0.00e+00;  
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

Db 1 atgagatgctgattcttttggctgttcacagccttctcgtggtatcctgtcgtatg 60  
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ORIGIN

Query Match 80.3%; Score 330; DB 56; Length 408;  
Best Local Similarity 92.0%; Pred. No. 0.00e+00;  
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

Db 1 atgagatgctgattcttttggctgttcacagccttctcgtggtatcctgtcgtatg 60  
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Query Match 80.3%; Score 330; DB 56; Length 408;  
Best Local Similarity 92.0%; Pred. No. 0.00e+00;  
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

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ORIGIN

Query Match 80.3%; Score 330; DB 56; Length 408;  
Best Local Similarity 92.0%; Pred. No. 0.00e+00;  
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

Db 1 atgagatgctgattcttttggctgttcacagccttctcgtggtatcctgtcgtatg 60  
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exon

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exon

BASE COUNT 99 a 109 c 92 g 108 t

ORIGIN

Jul 8 08:51

US-08-137-117B-30.rge

4

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 399)  
AUTHORS Iwasaki, Y., Takabatake, H., Shinji, T., Monestier, M. and Ferrone, S.  
TITLE Structural profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic system

JOURNAL Eur. J. Immunol. 24 (11), 2874-2881 (1994)

MEDLINE 95045941

COMMENT NCBI gi: 309346

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/sub\_species="domesticus"  
/cell\_type="hybridoma"  
/dev\_stage="adult"  
/sequenced\_mol="cDNA to mRNA"  
/sex="male"  
/tissue\_type="hyperimmunized spleen"  
<1..43  
1..>399  
/standard\_name="anti-HLA-DQ3 monoclonal antibody"  
/note="NCBI gi: 309347"  
/codon\_start=1  
/product="immunoglobulin heavy chain"  
/translation="MRVLLILLILFTAPPGILSDVQLQESGRLVLPKPSQSLSLTCTVTG  
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362..399

exon

CDS

BASE COUNT 93 a 107 c 94 g 105 t

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Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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exon

exon

exon

BASE COUNT 93 a 107 c 94 g 105 t

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Query Match 78.6%; Score 323; DB 56; Length 399;  
Best Local Similarity 96.3%; Pred. No. 0.00e+00;  
Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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exon

exon

exon

BASE COUNT 93 a 107 c 94 g 105 t

ORIGIN

Query Match 78.6%; Score 323; DB 56; Length 399;  
Best Local Similarity 96.3%; Pred. No. 0.00e+00;  
Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Best Local Similarity 96.3%; Pred. No. 0.00e+00;  
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exon

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BASE COUNT 93 a 107 c 94 g 105 t

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Query Match 78.6%; Score 323; DB 56; Length 399;  
Best Local Similarity 96.3%; Pred. No. 0.00e+00;  
Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 1 atgagatgctgattcttttggctgttcacagccttctcgtggtatcctgtcgtatg 60  
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exon

exon

exon

BASE COUNT 93 a 107 c 94 g 105 t

ORIGIN



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Qy 181 GGAACAAACTGAGTGGATGGCTACATAAGTTACAGTGGTATCACTTACCTACACCCA 240

Db 241 tctctcaaaagtcaatctctatcactcgagacacatccaaagaccaggtctctcgcag 300
Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGACCAGTTCCTCTACAG 300

Db 301 ttgaattctgtactactgaggacagccacatattactgtgcaaaat 349
Qy 301 TTGAATTCGTCACTACTCGGACACAGCTCCACATATTACTGTGCAAGAT 349

RESULT 3
LOCUS MMIGVHR2 450 bp RNA ROD 07-MAY-1992
DEFINITION Mouse mRNA for immunoglobulin heavy chain variable region.
ACCESSION X05878 Y00330
KEYWORDS constant region; Ig heavy chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 450)
AUTHORS Grant, F. J.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-1987) to the EMBL/GenBank/DBJ databases. Dr.
Francis Grant, Zymogenetics, Inc., 2121 North 35th Street, Seattle,
Wa 98103, USA
REFERENCE 2 (bases 1 to 450)
AUTHORS Grant, F. J., Levin, S. D., Gilbert, T. and Kindsvogel, W.
TITLE Improved RNA sequencing method to determine immunoglobulin mRNA
sequence
JOURNAL Nucleic Acids Res. 15 (13), 5496 (1987)
MEDLINE 87260030
COMMENT NCBI gi: 52526
FEATURES
source
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/organism="Mus musculus"
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/notes="variable region (AA 1-137)"
CDS
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BASE COUNT 116 a 126 c 92 g 116 t
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Matches 365; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Qy 61 CAGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACTCG 120

Db 124 actgtcactggctactcactcacctgggtgtatatacctggcactggatccggcagttcca 183
Qy 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGGAGTTTCCA 180

Db 184 ggaataaattggaatggatggctacatcacactacagtggttaacactgactttcaacca 243
Qy 181 GGAACAACAACTGGAGTGGATGGGCTACATGAAGTTACAGTGGTATCACTTACCAACCA 240

Db 244 tctctcaaaagtcaatctctatcactcgagacacatccaaagaccaggtctctcgcag 303
Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGACCAGTTCCTCTACAG 300

Db 304 ttgaattctgtactgagacagccacatattactgtgcaagaggtatggtaac 363
Qy 301 TTGAATTCGTCACTACTCGGACACAGCTCCACATATTACTGTGCAAGATCCCTAGCTCG 360

Db 364 tactatgctgactactgggttcaagaaacctcagtcacgtctctcca 414
Qy 361 ACTACGGCTATGGACTACTGGGGTCAGGACCTCAGTCACCGTCTCTCTCA 411

RESULT 4
LOCUS MMU05284 417 bp mRNA ROD 15-FEB-1995
DEFINITION Mus musculus BALB/c/J immunoglobulin heavy chain complete variable
region (Igh) mRNA, partial cds.
ACCESSION U05284
KEYWORDS .
SOURCE mouse.
ORGANISM Mus musculus
Eucaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Rodentia; Myomorpha; Muridae; Mus.
REFERENCE 1 (bases 1 to 417)
AUTHORS Tempest, P. R., White, P., Buttle, M., Carr, F. J. and Harris, W. J.
TITLE Humanized and chimerized monoclonal antibodies against the
glycoprotein gB of human cytomegalovirus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 417)
AUTHORS Tempest, P. R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-1994) Phillip R. Tempest, ICOS Corporation, 22021
20th Ave SE, Bothell, WA 98021, USA
COMMENT NCBI gi: 463457
FEATURES
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/clone_lib="Lambda HCV37"
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/codon_start=1
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/product="anti-cytomegalovirus-gB immunoglobulin heavy
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Best Local Similarity 95.4%; Pred. No. 0.00e+00;

Matches 330; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db 301 ttgtattctgtgaactgaggaacagccacatatattactgtgcaa 346

|||||

Qy 301 TTGAATTTCTGTACTTGGGACAGCTCCACATATTACTGTGCAA 346

RESULT 5

LOCUS MUSIGHQOC 402 bp mRNA ROD 28-APR-1995

DEFINITION Mouse Ig rearranged H-chain mRNA V-region, 5' end of cds.

ACCESSION L20957

KEYWORDS V-region; anti-HLA antibody; antibody;

immunoglobulin heavy chain; monoclonal antibody; processed gene.

SOURCE Mus musculus (strain BALB/c, sub species domesticus) male adult

hyperimmunized spleen cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 402)

AUTHORS Iwasaki,Y., Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S.

TITLE Structural profile of idiotype, anti-idiotypic and

anti-anti-idiotypic monoclonal antibodies in the HLA-DQ3 antigenic

system

JOURNAL Eur. J. Immunol. 24 (11), 2874-2881 (1994)

MEDLINE 95045941

COMMENT NCBI gi: 309348

FEATURES Location/Qualifiers

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/strain="BALB/c"

/sub species="domesticus"

/cell\_line="S01"

/cell\_type="hybridoma"

/dev\_stage="adult"

/sequenced\_mol="cDNA to mRNA"

/sex="male"

/tissue\_type="hyperimmunized spleen"

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/standard\_name="anti-HLA-DQ3 monoclonal antibody"

/note="NCBI gi: 309349"

/codon\_start=1

/product="immunoglobulin heavy chain"

/translation="MRVLIILLWLFATPGLISDVQLQESGPLVRPSQSLSLTCTVTG

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44..348

349..359

360..402

BASE COUNT 93 a 111 c 93 g 105 t

ORIGIN

Query Match 76.2%; Score 313; DB 56; Length 402;

Best Local Similarity 95.1%; Pred. No. 0.00e+00;

Matches 330; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db 1 atgagagctgattcttttggctgttcacagcctttctcgtatcctgtctgatgtg 60

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Qy 121 ACTGTCACTGGCTACTCAATCACCAGTCATGCTGCGAGCTGGATCCGGCAGTTTCCA 180

Db 181 ggaacaaactggagtgatgggtctacataagctacagtggttagcactggctacacaacca 240

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Qy 181 GGAAACAACCTGGAGTGGATGGGCTACATAGTTACAGTGGTATCATTACTTACAAACCCA 240

Db 241 tcgctcaaaagtgaatctctacatcgagacacatccaagaacagttctcctgcag 300

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Qy 241 TCTCTCAAAAGTCGAATCTTATCACTCGAGACACATCCCAAGACCACTTCTCTCTACAG 300

Db 301 ttgaattctgtgactactgaggaacagccacatatattactgtgcaag 347

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Qy 301 TTGAATTTCTGTACTTGGGACAGCTCCACATATTACTGTGCAAG 347

RESULT 6

LOCUS MUSTCHXX 460 bp mRNA ROD 26-MAR-1994

DEFINITION Mouse Ig rearranged gamma-chain mRNA, clone AN02g.

ACCESSION M19894 J03832

KEYWORDS C-region; immunoglobulin gamma-chain; immunoglobulin heavy chain;

processed gene.

SOURCE Mus musculus (strain BALB/c, sub species domesticus) cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 54)

AUTHORS Rule,G.S.

JOURNAL Unpublished (1988) Stanford U., Chem. Dept., Stanford CA 94305

REFERENCE 2 (bases 55 to 460)

AUTHORS Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.

TITLE Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-

JOURNAL bodies for NMR studies  
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)  
COMMENT 88234486  
Draft entry and computer-readable sequence [2] kindly submitted by  
G.Rule, 20-JUL-1988.

NCBI gi: 196225  
source Location/Qualifiers  
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/codon\_start=1  
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BASE COUNT 112 a 116 c 114 g 118 t  
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Matches 327; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Db 175 actgtcactggctactcaatcaccagtgattatgcttggaaactggatccgcgagtttcca 234  
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Qy 181 GGAACAAACTGGAGTGGATGGGTACATAAGTTACAGTGGTATCCTACTACAAACCCA 240  
  
Db 295 tctctcagaagtcgaactctatcactcgagacacatccaagaacagttcttctcgcag 354  
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Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGGACACATCCAAAGACAGTTCTTCTCAG 300  
  
Db 355 ttgaagtgcagtactactgaggacacagccacatatcttctgtgcaag 401  
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Qy 301 TTGAATTCGTGCTACTCTGGGACAGCTCCACATATTACTGTGCAAG 347

RESULT 7  
LOCUS MUSIGHAC 485 bp mRNA ROD 26-MAR-1994  
DEFINITION Mouse Ig rearranged gamma-chain mRNA, clone AN07g.  
ACCESSION M19899 J03832  
KEYWORDS C-region; immunoglobulin gamma-chain; immunoglobulin heavy chain;  
processed gene.

SOURCE Mouse (strain BALB/c) mature B cell, cDNA to mRNA, clone AN07g.  
ORGANISM Mus musculus  
Eukaryota; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 56)  
AUTHORS Rule,G.S.  
JOURNAL Unpublished (1988) Stanford U., Chem. Dept., Stanford CA 94305  
REFERENCE 2 (bases 57 to 485)  
AUTHORS Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.  
TITLE Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-  
bodies for NMR studies  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)  
MEDLINE 88234486  
COMMENT Draft entry and computer-readable sequence [2] kindly submitted by  
G.Rule, 20-JUL-1988.

NCBI gi: 194558  
source Location/Qualifiers  
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Db 177 actgtcactggctactccatcaccagtggttatagctggcactggatccgcgagtttcca 236  
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Qy 121 ACTGTCACTGGCTACTCAATCACCACTGATCATCCTGGAGCTGGATCCGGCAGTTTCCA 180  
  
Db 237 ggaacaaaactggaatggatgggtacatacactacagtggtagcactaacacaaacca 296  
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Qy 181 GGAACAAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCATCTACTACAAACCCA 240  
  
Db 297 tctctcaaaagtccaactctctatcactcgagacacatccaagaacagttcttctcgcag 356  
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Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGGACACATCCAAAGACAGTTCTTCTCTACAG 300  
  
Db 357 ttgaattctgtgactactgaggacacagccacatatattactgtgcaag 403

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11

Qy 301 TTGAATTCTGTGACTACTGGGACACGTCACATATTACTGTGCAAG 347

RESULT 8  
LOCUS MUSOHP138G 358 bp mRNA ROD 11-NOV-1992  
DEFINITION Mus musculus mRNA for Ig gamma chain precursor.  
ACCESSION D12726  
KEYWORDS Ig gamma chain; steroid specific antibody; variable region.  
SOURCE Mus musculus (strain BALB/c) hybridoma cell line OHP138.H8.1 mRNA.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Mammalia; Rodentia; Muridae.

REFERENCE 1 (bases 1 to 358)  
AUTHORS Sawada,J., Mizusawa,S., Terao,T., Naito,M. and Kurosawa,Y.  
TITLE Molecular characterization of monoclonal anti-steroid antibodies: primary structures of the variable regions of seven antibodies specific for 17alpha-hydroxyprogesterone or 11-deoxycortisol and their pH-reactivity profiles  
Mol. Immunol. 28, 1063-1072 (1991)

JOURNAL 92017897  
MEDLINE  
COMMENT Submitted (27-JUL-1992) to DDBJ by: Jun-ichi Sawada  
Dept. of Biochem. and Immunochem.  
National Institute of Hygienic Sciences  
1-18-1 Kamiyoga  
Setagaya, Tokyo 158  
Japan  
Phone: 03-3700-1141 x240  
Fax: 03-3707-6950.

FEATURES  
source NCBI gi: 220532  
Location/Qualifiers  
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CDS <1..>358  
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BASE COUNT 87 a 99 c 80 g 92 t  
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Db 61 acctgcactgtcactggctaccaccagtcattctgcctggaactgattccggcgag 120  
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Qy 115 ACTTCACCTTCACCTGGCTACTCAATCACCAGTGATCATGCCCTGGAGCTGATCCGGCAG 174

Db 121 ttctcaggaataagactggagtggtgggtacataagctacagtggtggcactggctac 180  
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Qy 175 TTTCAGGAACAACACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCACTACCTAC 234

Db 181 aacctctctcaaaagtcgaatctctatcacttcgagacacatccaagaaccagttcttc 240

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Qy 235 AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGACCATGTTCTTC 294

Db 241 ctgcagttgaattctgtgactactgagagacagccacacattactgttcaagaggtatc 300  
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Qy 295 CTACAGTTGAATTTCTGTGACTACTGGGACACAGCTGCCATATTACTGTCAAGATCCCTA 354

Db 301 tctattctctatgctggtactactgggtcaaggaaacctcagtcacctgtctctca 357  
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Qy 355 GCTCGGACTACGGCTATGGAAGTCTACTGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 411

RESULT 9  
LOCUS MUSOHP7D7G 358 bp mRNA ROD 11-NOV-1992  
DEFINITION Mus musculus mRNA for Ig gamma chain precursor.  
ACCESSION D12734  
KEYWORDS Ig gamma chain; steroid specific antibody; variable region.  
SOURCE Mus musculus (strain BALB/c) hybridoma cell line OHP7D7.2.3 mRNA.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Mammalia; Rodentia; Muridae.

REFERENCE 1 (bases 1 to 358)  
AUTHORS Sawada,J., Mizusawa,S., Terao,T., Naito,M. and Kurosawa,Y.  
TITLE Molecular characterization of monoclonal anti-steroid antibodies: primary structures of the variable regions of seven antibodies specific for 17alpha-hydroxyprogesterone or 11-deoxycortisol and their pH-reactivity profiles  
Mol. Immunol. 28, 1063-1072 (1991)

JOURNAL 92017897  
MEDLINE  
COMMENT Submitted (27-JUL-1992) to DDBJ by: Jun-ichi Sawada  
Dept. of Biochem. and Immunochem.  
National Institute of Hygienic Sciences  
1-18-1 Kamiyoga  
Setagaya, Tokyo 158  
Japan  
Phone: 03-3700-1141 x240  
Fax: 03-3707-6950.

FEATURES  
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Location/Qualifiers  
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BASE COUNT 90 a 98 c 82 g 88 t  
ORIGIN

Query Match 69.1%; Score 284; DB 57; Length 358;  
Best Local Similarity 91.1%; Pred. No. 6.68e-283;  
Matches 326; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

Db 1 gatgtgcagcttcaggagtcgggacctggcctgggtgaaccttctcagttctgtccctc 60  
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Qy 55 GATGTGAGCTTCAGGAGTCGGAGCCTGTCTCTGGTGAAGCCCTTCTCACTCTGTGCCCTC 114

Db 61 acctgcactgtcactgggtactcaatcaccagtcattctgtctggaactgggtccggcag 120

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115 ACCTGCACTGTCACCTGGCTACTCAATCACCAGTGATCATGCTGGAGTGATCCGGCAG 174
121 ttcccaagaacaactggatggatggctactaaactacagggtggcactggttac 180
175 TTTTCAGAAACAACTGGAGTGATGGCTACATAAGTTTACAGTGGTATCACTACCTAC 234
181 aaccatctctcaaaatcgaatctctcactcgaagacacatccaagaacaggattcttc 240
235 AACCATCTCTCABAAGTCGAATCTCTATCACTCGAGACACATCCCAAGAACCAAGTTCTTC 294
241 ctgcaattgaattctgtaccactgaggacagcgccacatatattactgtccaagagtaaat 300
295 CTACAGTTGAATTCGTGACTACTGGGACAGCTCCACATATTACTGTGCAAGATCCC-T 353
301 cgttactactatg-ctatggactactgggtcgaagaaacctcagtcacccgtctctcca 357
354 AECTCGGACTACGGCTATGGACTACTGGGTCAAGGAACCTCAGTCACCGCTCTCTCA 411

RESULT 10
LOCUS MUSIGHNUL1 434 bp DNA ROD 27-SEP-1994
DEFINITION Mus musculus germline Igh chain gene B allele, VDJ segment.
ACCESSION M28188
KEYWORDS J-segment; V-segment; germline; immunoglobulin;
immunoglobulin heavy chain.
SEGMENT 1 of 2
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) liver DNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 434)
AUTHORS Komori,T., Sugiyama,H. and Kishimoto,S.
TITLE A novel VHDJH to JH joining that induces H chain production in an
Ig-null immature B cell line
JOURNAL J. Immunol. 143 (3), 1040-1045 (1989)
MEDLINE 89309739
COMMENT NCBI gi: 341844
FEATURES
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380..391
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401..434
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Best Local Similarity 96.4%; Pred. No. 6.68e-283;
Matches 295; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db      92  ggtatcctgtctgatgtcgagcttcaggagtcggagcctggctggctggtgaaacctctcag 151
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Qy      43  ggtatcctgtctgatgtcgagcttcaggagtcggagcctggctggctggtgaaacctctcag 102

Db      152  tctctgtccctcaacctgcactgtcaactggctactcaatcaaccagtgattatgcttggagac 211
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Qy      103  TCTCTGTCCCTCAGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 162

Db      212  tggatcggcgagttccaggagaactcgagtgatgggtacataaagctacagtggt 271
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Db      272  agcactagttacaaccatctctcaaaagtcgaatctctatcaactcgagacacatccaag 331
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Qy      223  ATCACTACCTACACCCATCTCTGAAAGTCGATCTCTATCACTCGAGACACATCCAG 282

Db      332  aaccagttcttctgcagttgaattctgtgactactgagcacagcacatattactgt 391
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Qy      283  AACCAAGTTCTTCTACAGTTGAATTCTGTGACTACTGGGACACGTCACATATTACTGT 342

Db      392  gcaaga 397
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Qy      343  GCAAGA 348
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RESULT 11
LOCUS      Mouse Ig rearranged mu-chain gene V/D/J2 region from LB8 hybridoma,
DEFINITION anti-DNP, clone LB8-3.
ACCESSION MI3050
KEYWORDS   D-region; J-region; V-region; immunoglobulin heavy chain;
immunoglobulin mu-chain; processed gene.
SOURCE     Mus musculus (strain BALB/c, sub species domesticus)
            P.pneumotropica-specific anti-DNP hybridoma DNA.
ORGANISM   Mus musculus
            Eukaryote; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE  1 (bases 1 to 492)
AUTHORS   Dzierzak,E.A., Janeway,C.A.Jr., Richard,N. and Bothwell,A.L.M.
TITLE      Molecular characterization of antibodies bearing ID-460: The
            structure of two highly homologous V-H genes used to produce
            idiotype positive immunoglobulins
JOURNAL    J. Immunol. 136, 1864-1870 (1986)
MEDLINE    86141759
COMMENT    NCBI gi: 195342
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Matches 294; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy      43  ggtatcctgtctgatgtcgagcttcaggagtcggagcctggctggctggtgaaacctctcag 102
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Db 193 tctctgtccctcacctgcaactgctactggctactcaatcaccagtgattatgcttgaac 252  
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Db 253 tggatcggcaggttccaggaacaaactggagtggatggctacataaagctacagtgg 312  
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Qy 283 AACCAGTTCTTCTTACAGTTGAATTTCTGACTACTGGGACACGTCACATATTACTGT 342  
|||||  
Db 433 gcaaga 438  
|||||  
Qy 343 GCAAGA 348  
|||||

RESULT 12  
LOCUS MUSIGLAM 357 bp mRNA ROD 15-DEC-1988  
DEFINITION Mouse IgM H-chain lambda rearranged anti-Dns hybridoma VDJ1 region  
from family 36-60 mRNA.  
ACCESSION M15231  
KEYWORDS C-region; V-region; immunoglobulin heavy chain;  
immunoglobulin lambda; immunoglobulin lambda-2.  
SOURCE Mouse (strain Balb/c) hybridoma mRNA, clone DF8-611.1.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 357)  
AUTHORS Chua, M.-M., Goodgal, S.H. and Karush, F.  
TITLE Germ-line affinity and germ-line variable-region genes in the B  
cell response  
J. Immunol. 138, 1281-1288 (1987)  
MEDLINE 87110678  
COMMENT NCBI gi: 197675  
FEATURES  
source  
1..357  
/organism="Mus musculus"  
BASE COUNT 87 a 101 c 82 g 87 t  
ORIGIN Chromosome 16.

Query Match 67.9%; Score 279; DB 56; Length 357;  
Best Local Similarity 89.1%; Pred. No. 3.70e-277;  
Matches 318; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Db 1 gatgtcagcttcaggagccggagactggctggtaaaccttctcagctctgtccctc 60  
|||||  
Qy 55 GATGTGCAGCTTCAGGATGGGACCTCTCTGGTGAAGCCTTCTCAGTCTGTGCTC 114  
|||||  
Db 61 acctgcagctcactggctactcaatcaccagtcgattatgcttggaaactggatccggag 120  
|||||  
Qy 115 ACCTGCAGCTCAGTGGCTACTCATATACCAGTGATATATGCCTGGAGCTGGATCCGGAG 174  
|||||  
Db 121 ttctcaggaaacaaactggagtggatggctacataaagctacagtggtagcactagctac 180  
|||||  
Qy 175 TTTCAGGAACAAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCATACCTAC 234  
|||||  
Db 181 aaccatctctcaaaagtcgaatctctatcaactcgagacacatccaagaaccagttctc 240  
|||||

Qy 235 AACCATCTCTCAAAAGTCGAATCTCTATCACTCGACACATCCAGAACACGTTCTTC 294  
Db 241 ctgagttgaattctgtgactactgagacacagccacacatatattactgtcaagatgtccc 300  
|||||  
Qy 295 CTACAGTTCAATTCGTGACTACTGGGACAGCTCCACATATTACTGTCAAGATCCCTA 354  
Db 301 tatgattctctgactgtgctgtgggcgacagcagcaggtcacctgtctctca 357  
|||||  
Qy 355 CCTCGGACCTACCGGTATGCACTACTGGGTCAAGGAACCTCAGTACCGCTCTCCTCA 411  
|||||

RESULT 13  
LOCUS MUSIGHNOH 402 bp mRNA ROD 17-SEP-1991  
DEFINITION Mouse Ig active heavy-chain mRNA V-region.  
ACCESSION M64137  
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.  
SOURCE Mouse (strain BALB/c) B-cell hybridoma, cell line H146-24E9, CDNA  
to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Caton, A.J., Stark, S.E., Kavalier, J., Staudt, L.M., Schwartz, D. and  
Gerhard, W.  
TITLE Many variable region genes are utilized in the antibody response of  
balb/c mice of the influenza virus a/pr/8/34  
J. Immunol. 147, 1675-1686 (1991)  
MEDLINE 91349593  
COMMENT Specific for influenza virus A/PR/8/34 hemagglutinin.

NCBI gi: 195701  
FEATURES  
source  
Location/Qualifiers  
1..402  
/organism="Mus musculus"  
/strain="BALB/c"  
/sub\_species="domesticus"  
/cell\_line="H146-24E9"  
/cell\_type="B-cell hybridoma"  
/sequenced\_mol="cDNA to mRNA"  
<1..>402  
/note="NCBI gi: 195702"  
/codon\_start=1  
/product="Ig heavy chain"  
/translation="FFWCLTFAPGLSDVQLQESGPULVKPQSLSLTCVTGYSIT  
SGYSWHWIRQFPNGKLEMGYIHVSGTKYNPISKSAISITRDTSKNOFFLQINSVTT  
EDTATVYCARDDTYFDYMGQGTTLTVSSAKRH"  
BASE COUNT 104 a 113 c 81 g 104 t  
ORIGIN

Query Match 66.7%; Score 274; DB 56; Length 402;  
Best Local Similarity 91.3%; Pred. No. 2.03e-271;  
Matches 303; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 5 ttgtgtgcctgtccacagccttctcgtatctgtctgtgatgtgcagcttcaggagtca 64  
|||||  
Qy 17 TTTTGTGGCTGTTCACAGCCTTCTCGTATCCTGCTGATGTCAGCTTCAGGAGTCGG 76  
|||||  
Db 65 gacctgacctggtgaacacctctcagtcactcttcaactcacctgcactgtcactggctact 124  
|||||  
Qy 77 GACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCCTGCAGCTGCTGCTACT 136  
|||||  
Db 125 ccatcaccaagtggttatagctggcaactggatccggcagtttccaggaaacaaactggaat 184  
|||||  
Qy 137 CAAATCAACAGTGATCATGCTCGAGCTGGATCCGGCAGTTTCCAGGAACAAACTGGAGT 196  
|||||



Query Match 66.2%; Score 272; DB 56; Length 470;  
Best Local Similarity 84.9%; Pred. No. 4,00e-269;  
Matches 349; Conservative 0; Mismatches 59; Indels 3; Gaps 2;  
Db 56 atgaagattgttgadtctgtttacactcttgacagcattctctgtatctctgtatcta 115

[illegible]



361 -ACTACGGCTATGGACTACTCGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411

Search completed: Mon Jul 8 09:02:07 1996  
Job time : 289 secs.

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	411	100.0	411	5	Q30756	pPM-hl.	8.03e-269
2	265	64.5	720	7	Q40462	Fv(TU27) .	1.36e-164
3	256	62.3	378	4	Q25667	Sequence of the anti-	3.28e-158
4	255	62.0	714	12	Q67358	Anti-trascelide 02/01	1.68e-157
5	253	61.6	639	13	Q80291	Monoclonal antibody 2	4.39e-156
6	253	61.6	836	11	Q66698	Sequence of the singl	4.39e-156
7	235	57.2	351	1	Q06214	VH domain of antibody	2.41e-143
8	217	52.8	830	5	Q30716	Sequence of PCR produ	1.23e-130
9	213	51.8	798	5	Q30706	Sequence of Clone 21b	8.10e-128

## ALIGNMENTS

RESULT	1	
ID	Q30756	standard; cDNA; 411 BP.
AC	Q30756;	
DT	30-MAR-1993	(first entry)
DE	pPM-hl.	
DE	Human;	antibody; interleukin-6; receptor; IL-6R; light chain; L; H; H;
DE	heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;	
DE	plasmid; pPM-K3; pPM-hl; ss.	
OS	Synthetic.	
Key	Location/Qualifiers	
FT	sig_peptide	1..54
FT	/*tag= a	
FT	mat_peptide	55..411
FT	/*tag= b	
FT	WO9219759-A.	
PD	12-NOV-1992.	
PPF	24-APR-1992;	J00544.
PPR	25-APR-1991;	JP-095476.
PPR	19-FEB-1992;	JP-032084.
PPR	(CHUS ) CHUGAI SEITAKU KK.	
PPI	Bendig MM, Jones ST, Saldana JW, Sato K, Tsuchiya M;	
DR	WPI; 92-398882/48.	
DR	P-PSDB; R28671.	
DR	Reconstituted human antibody to human interleukin-6 receptor -	

PT has low antigenicity and contains mouse V-region complementarity

PT Determining regions

PS Disclosure; Page 122-123; 207pp; Japanese.

CC The sequences given in Q30755-56 were used in example to illustrate the production of a human antibody which recognises human

CC interleukin-6 receptor (IL-6R). The antibody comprises light (L)

CC chain and heavy (H) chain variable regions which were derived from a

CC mouse monoclonal antibody produced from the hybridoma PM1 which

CC contained the plasmids pPM-k3 and pPM-h1.

SQ Sequence 411 BP; 95 A; 114 C; 92 G; 110 T;

Query Match 100.0%; Score 411; DB 5; Length 411;

Best Local Similarity 100.0%; Pred. No. 8.03e-269;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 atgagagtgctgattcttttgggtgtcttcacagcctttcctgggtatcctgtctgatgtg 60

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 1 ATGAGAGTCTGATCTTTTGGCTGTTCACAGCGCTTCTCGTATCTGTCTGATGTG 60

Db 61 cagcttcaggagtcggagcctgtcctgttggaagccttcacgtctctgtccctcacctgc 120

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 61 CAGGTTTCAGAGTCGGGACCTCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120

Db 121 actgtcaactggtactcaatcacagtcgactgctgctggagtcggagtcggagtttccaa 180

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 121 ACTGTCACTGGCTACTCAATCACAGTCATCGCTGGAGTCGATCGGCGGCGATTTCCA 180

Db 181 ggaacaaactggagtggtgggtacataagttacagtggtgtatcactacacaccca 240

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 181 GGAACAAACTGGAGTGGATGGGTACATAAGTTACAGTGGTATCACTACTACACCCA 240

Db 241 tctctcaaaagtcgaatctctatcactcgagacacatccaagaaccagcttctctacag 300

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 241 TCTCTCAAAGTCAATCTCTATCACTCGACACATCCAAAGACCACTTCTCTCTACAG 300

Db 301 ttgaattctgtactactgggacacgtccacatattactgtcaagatccctagctcgg 360

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 301 TTGAATTTCTGTACTCTGGGACACGTCCACATATTACTGTGCAAGATCCCTACTCGG 360

Db 361 actacggtctatggactactgggtcaagaaacctcagtcacgtctctcca 411

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 361 ACTACGGCTATGGACTACTGGGGTCAAGAACCTCAGTCACCGTCTCTCTCA 411

#### RESULT 2

ID Q40462 standard; DNA; 720 BP.

AC Q40462;

DT 20-AUG-1993 (first entry)

DE Fv(TU27).

KW pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;

KW heavy; beta; chain; interleukin; IL-2; receptor; inhibition;

KW immunomodulator; immunosuppressant; graft rejection; allergy;

KW autoimmune disease; leukemia; cyclosporin; ss.

OS Homo sapiens.

PN EP-539748-A.

PD 05-MAY-1993.

PF 03-SEP-1992; 116746.

PR 03-OCT-1991; JP-256335.

PA (AJIN ) AJINOMOTO KK.

PI Hamuro J, Shinamura T, Taki S;

DR WPI; 93-145163/18.

DR P-PSDB; R34510.

PT Polypeptide(s) which bind H chain of human IL-2 receptors - for

PT treating inflammatory, allergic and auto-immune disorders,

PT leukaemias etc.

PS Claim 6; Page 20; 27pp; English.

CC The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express polypeptides consisting only of the V regions were purified and

CC sequenced. The polypeptides are capable of binding to the beta

CC chain of IL-2 receptor and of inhibiting the binding of IL-2 to the

CC receptor. They are useful as immunomodulators and

CC immunosuppressants, e.g. to prevent graft rejection or to treat

CC inflammatory allergic and autoimmune diseases, or leukemia. Unlike

CC cyclosporin etc. they are both effective and safe.

SQ Sequence 720 BP; 186 A; 188 C; 170 G; 176 T;

Query Match 64.5%; Score 265; DB 7; Length 720;

Best Local Similarity 90.7%; Pred. No. 1.36e-164;

Matches 312; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

Db 380 agagctctggagctggcctggtgaaacctctcagctctctgctccctcacctgcactgtca 439

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 68 AGGAGTCGGGACCTGTCTGCTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGCACGTGCA 127

Db 440 ctggctaccacatccaccagtgattatgctgggagtcggatccggcgagtttccagaagaa 499

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 128 CTGGCTACTCAATCACCACTGATCATGCTGGAGCTGGATCGGCGAGTTTCCAGGAACA 187

Db 500 aactggagtgagtggtcactgaagctacagtgtagcagtcgactgactacacacccatctctca 559

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 188 AACTGGAGTGGATGGGCTACATATAGTTAGTGTATCACTACTACACACCATCTCTCA 247

Db 560 aaagtcgaatctctatcagtcgagacacacatccaagaaccagttcttctcgagttgaatt 619

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 248 AMAGTCGAATCTTATCACTCGACACATCCAAAGAACCCGTTTCTCTACAGTTGAATT 307

Db 620 ctgtgactactgagacacagccacacatattactgtgcaagagg--tggtttccctctatg- 676

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 308 CTGTGACTACTGGGGACACGTCACATATTACTGTGCAAGATCCCTAGCTCGGACTACGG 367

Db 677 ctatgactactgggtcaaggacacagtcacagtcacgtctctctca 720

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 368 CTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGCTCTCTCTCA 411

#### RESULT 3

ID Q25667 standard; cDNA; 378 BP.

AC Q25667;

DT 28-DEC-1992 (first entry)

DE Sequence of the anti-urokinase antibody kappa variable region (VK)

DE cDNA

KW Chimeric monoclonal antibody; anti-urokinase antibody; PCR;

KW antithrombotic agent; myocardial infarction therapy; ss.

OS Mus musculus.

FT Key Location/Qualifiers

FT sig peptide 1..9

FT /\*tag= a 10..378

FT mat peptide b 1..27

FT misc feature c 18..32

FT /\*tag= d 340..371

FT misc feature 340..371

FT /\*tag= e 3' mVH primer

FT misc\_feature 356..371  
FT /\*tag= f  
FT /label= JH01 primer  
PN EP-491351-A.  
PD 24-JUN-1992.  
PR 17-DEC-1991; 121591.  
PR 18-DEC-1990; JP-413829.  
PR 11-NOV-1991; JP-294464.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
PI Iwasa S, Taka H, Watanabe T, Tada H;  
DR WPI; 92-209528/26.  
DR P-P5DP; R24722.  
PT Chimeric monoclonal antibodies - contain anti-human fibrin  
PT antibody light and heavy chain variable and constant for treating  
PT thrombotic conditions e.g. myocardial infarction  
PS Example; Figure 15; 87pp; English.  
CC Poly(A)+ RNA was pred. from mouse anti-urokinase  
CC antibody-producing hybridoma UK1-3 cells. Using this poly(A) RNA as  
CC a template, an anti-urokinase antibody VK cDNA was amplified with  
CC the mC-kappa primer as primer for first strand synthesis, and the  
CC 3'mV-kappa and 5'mV-kappa primers as primers for the PCR. The  
CC amplified fragment was restriction digested and ligated into a  
CC restriction fragment of pTB1423 to give an anti-urokinase antibody  
CC VK cDNA contg. plasmid pTB1456. The sequence of this plasmid is  
CC given in Q25667. The cDNA is a functional VK gene. The sequence of  
CC the primer (mC-gamma-1) is given in Q25689.  
SQ Sequence 378 BP; 92 A; 100 C; 91 G; 95 T;  
  
Query Match 62.3%; Score 256; DB 4; Length 378;  
Best Local Similarity 93.2%; Pred. No. 3.28e-158;  
Matches 276; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
  
Db 9 ttagggtcaactagtgagctcgagctggcctggtgaaaccttctcagctctctgtcctc 68  
QY 54 TGATGTGCGAGCTTGAGGAGTGGGACCTGTCTGTGTGAGCGCTTCATGCTCTGTCCT 113  
  
Db 69 cactgcactgtcactggctactcaatcaccagtgattatgctggaactggatccgca 128  
QY 114 CACCTGCACCTGTCACTGGCTACTCAATCACCACTGATCATGCTGAGCTGGATCCGCA 173  
  
Db 129 gttccaggaaacaaactggagtgatgggtacataaactacagtggtaccactagtta 188  
QY 174 GTTCCAGGAACAAACTGGAGTGGATGGCTACATAAGTTACAGTGTATCACTACCTA 233  
  
Db 189 caaccatctcctcaaaagtgaattctctatcactcgagacacatccataaaccagtttt 248  
QY 234 CAACCGATCTCTCAAGTGGATCTTATCACTCGACACATCCAGAACCACTGCTT 293  
  
Db 249 cctgcagtgaattctgtgactcttgaggacactgctccacatattactgtgcaagat 304  
QY 294 CCTAGATTGAATCTGTGCTACTTGGGGACACGTCACATATTACTGTGCAAGAT 349  
  
RESULT 4  
ID Q67358 standard; DNA; 714 BP.  
AC Q67358;  
DT 27-MAR-1995 (first entry)  
DE Anti-traseolide 02/01/01 scFv.  
KW Binding protein; immobilization; chimeric protein;  
KW anchoring protein; Saccharomyces cerevisiae; pUR4143;  
KW mask fragrance; traseolide; polymerase chain reaction;  
KW PCR; amplification; primer; light chain; hybridoma; scFv;  
KW single chain antibody; monoclonal antibody; ds.  
OS Synthetic.

PN W09418330-A.  
PD 18-AUG-1994.  
PF 10-FEB-1994; E00427.  
PR 10-FEB-1993; EP-200350.  
PA (UNIL ) UNILEVER NV.  
PA (UNIL ) UNILEVER PLC.  
PI De Geus P, Erenken LGJ, Klis FM, Toeschka HY, Verrips CT;  
DR WPI; 94-279751/34.  
PT Immobilised binding proteins for specific cpds - obtd. by  
PT expressing chimeric proteins comprising the binding protein and a  
PT cell wall-anchoring protein in host cells  
PS Disclosure; Page 35; 78pp; English.  
CC Valuable compounds are isolated from complex mixtures by use of  
CC immobilized ligands composed of an anchoring protein and a binding  
CC protein. A gene encoding such a chimeric protein that will anchor  
CC in the cell wall of a lower eukaryote, e.g. S. cerevisiae, and which  
CC binds traseolide with high specificity, was constructed using plasmid  
CC pUR4143. This plasmid contains a gene encoding an scFv-TRAS  
CC fragment of anti-traseolide antibody 02/01/01 (Q67358) obtained by  
CC PCR amplification of hybridoma cDNA using primers Q67353-54 for  
CC the heavy chain, and primers Q67355-56 for the light chain.  
SQ Sequence 714 BP; 174 A; 188 C; 178 G; 174 T;  
  
Query Match 62.0%; Score 255; DB 12; Length 714;  
Best Local Similarity 93.8%; Pred. No. 1.68e-157;  
Matches 273; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
  
Db 1 ctgcaggagctggacctggcctggctgaaaccttctcagctctctgtcctcactgcact 60  
QY 64 CTTCCAGGAGTCGGGACCTCTCTGTTGAAGCTTCTCAGTCTCTGCTCCTCAGCTGCAC 123  
  
Db 61 gtcaactgctactcaatcaccagtgatttgcctggaaactggatccggcagtttccagg 120  
QY 124 GTCACTGGCTACTCAATCACCACTGATCATGCTGGAGCTGGATCCGGCAGTTTCAGGA 183  
  
Db 121 aaccaactggagtgatggctacatgaactgaactggtagcactagctacaacccatct 180  
QY 184 AACAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCATCTACACACCCATCT 243  
  
Db 181 ctcaaaagtccaatctctcactcgagacacatccaagaaccagttcttctcagcttg 240  
QY 244 CTCAAAAGTCCGAATCTTATCACTCGACACATCCAAAGAACAGTTCTTCTTACAGTTG 303  
  
Db 241 aattctgtactactgagacagacagcacatattactgtgcaacgtcccta 291  
QY 304 AATTCTGTACTACTGGGACACGCTCCACATATTACTGTGCAAGATCCCTA 354  
  
RESULT 5  
ID Q80291 standard; DNA; 639 BP.  
AC Q80291;  
DT 08-JUL-1995 (first entry)  
DE Monoclonal antibody 28C5 heavy chain.  
KW CD14 receptor; monoclonal antibody; 28C5; hybridoma;  
KW antiseptic; therapeutic; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT mat\_peptide 1..639  
FT /\*tag= a  
FN W09428025-A.  
PD 08-DEC-1994.  
PF 27-MAY-1994; U05898.  
PR 28-MAY-1993; US-070160.  
PA (SCRI ) SCRIPES RES INST.



CC	for MAb C and D.
SQ	Sequence 351 B

Query Match 57.2%; Score 235; DB 1; Length 351;  
Best Local Similarity 91.2%; pred. No. 2.41e-143;  
Matches 260; Conservative 0; Mismatches 25; Indels

**Db**      1    ctgcaggagtcaggacctgacctggtgaaacottctcagtcactttcacctcacctgacct    60  
         ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
**Ov**      64    cttcaggagtcgggaactgtcctggtaagcccttcagtctctgtgccctcaactcgacct    123

Db 61 gt cactggctactccatcaccagtggttatagctggaactggaatccggcagtttccagga 120

Ov 124 gtcactggctactccatcaccagtggaatgctggaactggaatccggcagtttccagga 183

Db 121 acaaaactggaatgtagtgggtacatcacagtacagtggtatcactaacctaacacctctc 180

Qw 184 AACAACTCGGACTCGATCGCGCTACATACCTTACATCGCTATACATCTACATACACCTATCT 243

Db 181 ctcaaagtcgaatctctatcaactcgagacacatccaagaccagttcttctcaggttg 240  
ctcaaaagtcgaatctctatcaactcgagacacatccaagaccagttcttctcaggttg 240  
ctcaaaagtcgaatctctatcaactcgagacacatccaagaccagttcttctcaggttg 240  
ctcaaaagtcgaatctctatcaactcgagacacatccaagaccagttcttctcaggttg 240

[illegible]

## RESULT 8

AC Q30714;  
DT 20-MAR-1993 (first entry)  
DE Sequence of PCR product linking the Fd sequence with the

DE	sequence
KW	Filamentous phage; coat protein membrane anchor domain; ss.
OS	Synthetic.

PD 29-OCT-1992.  
PF 10-APR-1992; U03091.  
PR 10-APR-1991; US-683602.

PA (SCRI ) SCRIPPS RES INST.  
PI Barbas C, Kang A, Lerner RA;  
DR WPI; 92-382106/46.

PT antibody, in its coat protein, useful for diagnostic assay, also  
PT new phage DNA libraries and mutagenic oligo:nucleotide primers  
PS Example: Page 196; 229pp; English.

the example concerns the preparation of a DNA segment encoding a portion of the fusion protein Fd-cpVIII. Fd comprises the VH and CHI chains. cpVIII is a filamentous phage coat protein membrane anchor domain. 030714 is the sequence of the PCR product linking the

CC FD sequence with the cpvIII sequence in frame in a 3' to 5'  
CC direction. The FD-cpvIII fusion product was then used in  
CC directional ligations for the construction of a pCBAR8-2b  
CC dicistronic phagemid expression vector.

SQL sequence	830 BF; 196 A;	240 C; 194 G;	200 I;
Query Match	52.8%;	Score 217;	DB 5; Length 830;
Best Local Similarity	82.8%;	Prod No. 1	230-130;

Matches 293; conservative 0; mismatches 38; indels 3; gaps 3  
Db 3 gtccagattctcagatctggacctggcctcgtgaaaccttctcagtcctctgtctctacc 62

58 GTGCGCTTACGGA GTCCGGA CCTGTCTCTGTGA GCCCTCTCAGTCTCTCTCCCTCACC 117

[illegible]

Db 123 ccaggaaacaactggaatggatgggctacataaagctacgacggtgtcaataagtatgat 182  
|||||  
Ov 178 CCAGGAACAACAACTGGAGTGGATGGGCTACATAAGTACACTGGTATCACTACCCTACAAC 237  
|||||

**Db** 183 ccattctcagaatcgaatctccatcactcgtagacatctatacaaatcagtttttcag 242  
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |  
**Ov** 238 CCATCTCTCAAAACTCGAATCTCTATCATCTCGAGACACATCCAGAACCACCTTCTCCTA 297

Db 243 aagttgattctgtgactcttgaggacacaggacaatatgactgttcaagagg--a-ct 299  
|||||  
Q<sup>u</sup> 208 CACATTCATATTCCTGCATCTATCCCGCCACACATCTCCACATATTCATCTCCATCC 357

[illegible]

RESULT 9

AC	Q30706;
DT	20-MAR-1993 (first entry)
DE	Sequence of Clone 21b expressing variable heavy (VH) and constant

Nitrophenylphosphonamide; NPN; ligand; receptor binding;  
immunoglobulin; light chain; heavy chain; ss.  
OS Synthetic.

PD 29-OCT-1992.  
PF 10-APR-1992; U03091.  
PR 10-APR-1991; US-683602.

PA (SCRI ) SCRIPPS RES INST.  
PI Barbas C, Kang A, Lerner RA;  
DR WPI; 92-382106/46.

antibody, in its coat protein, useful for diagnostic assay, also new phage DNA libraries and mutagenic oligo:nucleotide primers Example; Page 188; 229pp; English.

CC expressing the heavy (Fd consisting of VH and CH1) and light  
CC (kappa) chains (VL, CL) of antibodies targeted to the periplasm  
CC of *E. coli* for the assembly of heterodimeric Fab molecules. The DNA

homologues were prepared and inserted into a *uvrA* expression vector. VH and VL DNA homologues were then randomly combined on the same expression vector. Anti-nitrophenylphosphonamide (NPN) reactive heterodimer-producing digastric vectors were then selected.

CC Clone 2b is one of the plaques which reacted with rFN. The sequence  
CC of clone 2b Fd chain is given in Q30706. The sequence of the kappa  
CC light chain variable and constant regions are given in Q30707 and  
CC Q30708 respectively.

SQ sequence 198 BF; 190 A; 239 C; 179 G; 190 I;  
 Query Match 51.8%; Score 213; DB 5; Length 798;  
 Best Local Similarity 92.2%; Prod No 9 100-198;

Matches 291; Conservative 0; Mismatches 60; Indels 3; Gaps 0

Db 103 gtgaaactgtctgagtcaggacctggcctcgtgaaaccttcagtcctctgtctctcacc 162



```
Qy 58 GTGCAGCTTCAGGAGTCGGGACCTGCTGGTGAAGCCTCTCAGTCTCTGTCCCTCACC 117
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||||||
Db 163 tgctctgtcaactgactaccatccacagctgcttattactggaactggatccggcagttt 222
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||||||
Qy 118 TGCAGTCTCAGCTGGCTACTCAATCACCAGCTGATATGCCGTGAGCTGGATCGGCAGTTT 177
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||||||
Db 223 ccagaaacaactggaatggatgggtacataaagctacgacggtgtcaataagtatgat 282
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||||||
Qy 178 CCAGGAAACAACCTGGAGTGGATGGGTACATAAGTTACAGTGGTATACACTACCTACAAC 237
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||||||
Db 283 ccaatctcacaagaatcaatctccatcaactcgtgacacatctaaacaatcagttttccag 342
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||||||
Qy 238 CCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAGAACCAAGTCTTCCTCA 297
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||||||
Db 343 aagttgattctgtgactctgtgagcacaggaacatatgactgttcaagagg--a-ct 399
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Qy 298 CAGTTGAATTCGTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCT 357
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Db 400 agggcctctgctatggactactggggtcaaggaatttcagtcacccgtctctcca 453
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Qy 358 CGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||

RESULT 10
ID Q44642 standard; DNA; 798 BP.
AC Q44642;
DT 04-OCT-1994 (first entry)
DE Fd phage clone sequence comprising kappa light chain regions.
KW Expression; kappa light chain; antibody; expression vector;
KW bacteriophage; clone; Fd; ds.
OS Synthetic.
PN WO9405781-A.
PD 17-MAR-1994.
PF 03-SEP-1993; U08364.
PR 04-SEP-1992; US-941369.
PA (SCRI ) SCRIPS RES INST.
PI Lerner RA, Light JP;
DR WPI; 94-101186/12.
PT Filamentous phage comprising a heterologous polypeptide and a
PT hetero-dimer - is used to detect the presence of a preselected
PT ligand in a sample
PS Example 2f; Page 198; 237pp; English.
CC This synthetic sequence was packaged into the filamentous phage Fd.
CC It comprises kappa light chain variable and constant regions. The
CC clone encodes anti-NPN (Nitrophenylphosphonamide) reactive
CC heterodimers.
SQ Sequence 798 BP; 190 A; 238 C; 179 G; 191 T;

Query Match 51.8%; Score 213; DB 10; Length 798;
Best Local Similarity 82.2%; Pred. No. 8.10e-128;
Matches 291; Conservative 0; Mismatches 60; Indels 3; Gaps 2;

Db 103 gtgaaactgctcgagtcaggaaactggcctcggaacattctcagttctgtctctcacc 162
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Qy 58 GTGCAGCTTCAGGAGTCGGGACCTGCTGGTGAAGCCTCTCAGTCTCTGTCCCTCACC 117
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Db 163 tgctctgtcaactgactaccatccacagctgcttattactggaactggatccggcagttt 222
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Qy 118 TGCAGTCTCAGCTGGCTACTCAATCACCAGCTGATATGCCGTGAGCTGGATCGGCAGTTT 177
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Db 223 ccagaaacaactggaatggatgggtacataaagctacgacggtgtcaataagtattat 282
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Qy 178 CCAGGAAACAACCTGGAGTGGATGGGTACATAAGTTACAGTGGTATACACTACCTACAAC 237
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
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Db 283 ccaatctcacaagaatcgaaatctccatcaactcgtgacacatctaaacaatcagttttccag 342
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Qy 238 CCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACATCCAGAACCAAGTCTTCCTCA 297
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Db 343 aagttgattctgtgactctgtgagcacaggaacatatgactgttcaagagg--a-ct 399
||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Qy 298 CAGTTGAATTCGTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTAGCT 357
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Db 400 agggcctctgctatggactactggggtcaaggaatttcagtcacccgtctctcca 453
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||
Qy 358 CGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
||||| ||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| |||

RESULT 11
ID Q31365 standard; DNA; 438 BP.
AC Q31365;
DT 30-MAR-1993 (first entry)
DE pUC-RVh-PM1f-4.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KW complementarity determining region; mouse; monoclonal; hybridoma;
KW plasmid; polymerase chain reaction; amplify; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 12..425
FT sig_peptide 12..68
FT /*tag= a
FT /*tag= b
FT mat_peptide 69..425
FT /*tag= c
PN W09219759-A.
PD 12-NOV-1992.
PR 24-APR-1992; J00544.
PR 25-APR-1991; JP-095476.
PR 19-FEB-1992; JP-032084.
PA (CHUS ) CHUGAI SEIYAKU KK.
PI Bendig WM, Jones ST, Saldanha JW, Sato K, Teuchiya M;
DR WPI; 92-398882/48.
DR P-PSDB; R29014.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 142-3; 207pp; Japanese.
CC The sequences given in Q31360-61 and Q31365-66 are plasmids encoding
CC portions of monoclonal antibodies which were derived from mouse
CC hybridomas. The DNA encoding complementarity determining regions
CC (CDR's) was isolated by polymerase chain reaction. The antibodies
CC produced recognises human interleukin-6 receptor (IL-6R). The
CC hybridoma cells were transformed with plasmids containing fragments
CC of the antibody gene which caused the production of the antibody from
CC the hybridoma cells.
SQ Sequence 438 BP; 105 A; 123 C; 113 G; 97 T;

Query Match 40.6%; Score 167; DB 5; Length 438;
Best Local Similarity 72.6%; Pred. No. 1.45e-95;
Matches 268; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Db 57 ggtgtccatccccaggtccaaactcgaggagcaggtccaggtctgttgagacatgaccag 116
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 43 GGTATCCTCTGTGATGTGCAGCTTCAGAGTTCGGACCTGTCTCTGGTGAAGCCTTCAC 102
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 117 accctgagcctgacctgcacgtgtctggctactcaattaccagcagcatcatcctggagc 176
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 103 TCTCTGTCCCTCACCTGGACACTGTCATGTGGCTACTCTCAATCACCAGTGCATCATCGCTGGAGC 162
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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PPA	(NEWG-) NEW ENGLAND DEACONESS HOSPITAL CORP.
PI	Haseltine WA, Marasco WA, Posner ME, Sodroski JG;
PI	WPI; 93-214174/26.
DR	P-PSDB; R38669.
PT	DNA segments encoding monoclonal antibody - which binds
PT	and neutralises HIV, for treating AIDS, and for diagnosis
PT	monitoring HIV infection
PS	Disclosure; Page 62-63; 109pp; English.
CC	The nucleotide sequence of rearranged F105 Vh (Q42698)
CC	to two monoclonal antibodies (Ab26 - Q42702) and 768-D
CC	which by nucleotide sequence analysis, appear to use a
CC	Vh 71-4 gene (Q42697).
CC	Ab26 (Q42702) was derived from CD5+ B cells of a healthy
CC	represents a naturally occurring polypeptide antibody
CC	many antigens. Ab26 shares greatest sequence similarity
CC	Vh 71-4.
SQ	Sequence 351 BP; 72 A; 99 G; 81 T;

Query Match	39.4%;	Score 162;	DB 7;	Length 351;
Best Local Similarity	77.2%;	Pred. No. 4,41e-92;		
Matches	230;	Conservative 0;	Mismatches 68;	Indels 0; Gaps
Db	50	tctgtcccaggtgcagctgcaggagtcggggcccccaggactggtagccttcacagacc	1	
Qy	47	TCCTCTGTATGTCAGCTTCAGAGTCGGGACCTGTCTCTGGTGAAGCCTTCTCAGTCTC	1	
Db	110	tgtccctcacttgcactgtctctgtgtgctccactcagtagtggtattactggagctgga	1	
Qy	107	TGTCCCTCACCCTGCCACTGTCACTGGCTACTCAATCACCACTGATCATCCCTGGAGCTGGA	1	
Db	170	tcgcgcagcacccaggggaagggctggagtgagtggtgcacatatattacagtgggagca	2	
Qy	167	TGGCGCATTTTCAGGAAACAAACTGGAGTGGGTGACATACATGTTACACTGTTGTATCA	2	
Db	230	ccaactacaaccctccctcaagagtcgaagtgtccgatcatcagtgacagctctaaagacc	2	
Qy	227	CTACCTCAACCCATCTCTCAAAAGTCGAATCTCTATCACTCGACACATCAACAAGCC	2	
Db	290	agttctccctggaagctgagctctgtgacccgctcgggacaagggccgtgtattactgtgc	347	
Qy	287	AGTTCTTCTCAGATTGAATTTCTGTCACTACTGGGACAGCTCCAATATTACTGTGC	344	

RESULT	14	
ID	Q78966	standard; DNA; 624 BP.
AC	Q78966;	
DT	03-AUG-1995	(first entry)
DE	Human immunoglobulin Vh gene #28.	
KW	Primer; PCR; amplif;	human; immunoglobulin; variable; heavy chain;
KW	cosmid; placenta;	vector; pJB81; E.coli; mammalian; ds.
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	151..583
FT	/*tag= a	
FT	/product=	human immunoglobulin variable heavy chain
FT	intron	197..278
FT	/*tag= b	
FT	misc_signal	
FT	/*tag= c	584..586
FT	/note=	"miscellaneous signal, does not conform to
FT	terminator or splice site sequence"	
PN	W09426895-A.	
PD	24-NOV-1994.	
PD	10-MAY-1993;	J00603.

PR	10-MAY-1993; WO-J00603.
PA	(NISB) JAPAN TOBACCO INC.
PI	Honjo T. Matsuda F;
DR	WPI; 95-006791/01.
PT	P-PSDB; R66320.
PR	DNA fragment comprising human immunoglobulin Vh genes - for the
PT	production of human immunoglobulin in mammalian hosts
PS	Disclosure; Page 67-68; 130pp; Japanese.
CC	A series of genes (Q78939-79002) encoding human immunoglobulin variable
CC	heavy chains. The genes were isolated and cloned from a series of cosmid
CC	constructs; Y202; Y103; Y6; Y24; 3-31; M84; M118 and M131, by PCR
CC	amplification using primers Q78917-38. The genes are subdivided into 5
CC	families of Vh genes. The fragments cover a region of 800 kb. The DNA
CC	fragments were isolated from high molecular weight DNA from human
CC	placenta. The DNA was partially digested with TaqI restriction enzyme.
CC	The fragments were separated by gel electrophoresis and 35-45 kb fractions
CC	were collected. The fragments were ligated with ClaI-digested cosmid
CC	vector pCB81. The ligation products were in vitro packed and infected
CC	into E.coli 490A. The fragments were then subcloned by colony
CC	hybridisation. The Vh genes and the DNA fragments encoding them are
CC	useful in producing human immunoglobulin in mammalian hosts.
SQ	Sequence 624 BP; 141 A; 179 C; 168 G; 136 T;

Query Match	38.9%;	Score 160;	DB 13;	Length 624;
Best Local Similarity	76.5%;	Pred. No. 1.09e-90;		
Matches 231;	Conservative	0;	Mismatches 71;	Indels 0;
Gaps				
Db	282	tctgtccacggtgcagctgcagagctcgggcccgagactggtgaacgcttcoggacacc	341	
Qy	47	TCCTGTCTCATGTGCAGCTCAGACAGTCGGGACCTGCTCGTGTGAACCCCTTCCTCAGCTC	106	
Db	342	tgteccctcacctgcgctgtctctggttactccatcagcagtagtaactggtggggctgga	401	
Qy	107	TGTCCCTCACCCTGCAGCTGTCACTGGCTACTCAATCACCAAGTCATCGCTGGAGCTGGGA	166	
Db	402	tcggcagcgcgcccgaaaggagactggatggatgggtggtggtacactattatagatgggagca	461	
Qy	167	TCGGGAGTTCCTCAGGAAACAAACTGGAGTGGATGGGCTACATAAGTTACAGTGTGTATCA	226	
Db	462	cctactacaacccogtccctcaagagtgcagtcacactgtcagtagacacogtccgaagacc	521	
Qy	227	CTACCTACAGACCCATCTCTCAAAAGTCGAATCTATATCACTCGACACACATCCAGAAC	286	
Db	522	agttctccctgaagctgagctctgtgaccgcggtggacacggcgtgtattactgtgcga	581	
Qy	287	AGTTCTTCCTACATTGAAATTCTGTGACTCTGGGGACAGCTCCACATATTACTGTGCA	346	
Db	582	ga 583		
Qy	347	GA 348		

RESULT	15	
ID	Q42699	standard; DNA; 348 BP.
AC	Q42699;	
DT	01-NOV-1993	(first entry)
DE	VH411.	
DE	Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS;	
KW	CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;	
KW	chain; epitope; immune deficiency; ss.	
OS	Homo sapiens.	
Key	Location/Qualifiers	
FT	sig_peptide	1..57
FT	/*tag= a	

PT DNA segments encoding monoclonal antibody – which binds to gp120  
PT and neutralises HIV, for treating AIDS, and for diagnosing and  
PT monitoring HIV infection  
PS Disclosure: Page 56-58; 109pp; English.  
CC The nucleotide sequence of rearranged F105 Vh (Q42698) was compared  
CC to several similar germline Vh IV genes. F105 Vh shares greatest  
CC sequence similarity with germline Vh 71-4 (Q42697). Non-rearranged  
CC Vh IV germlines Vh 4.11 (Q42699), 4.15 (Q42700) and 4.16 (Q42701)  
CC that were identified by PCR amplification of genomic DNA from an  
CC adult healthy Caucasian donor, are most closely related to Vh 71-4  
SQ Sequence 348 BP; 72 A; 101 C; 97 G; 78 T;

Query Match	37.2%;	Score 153;	DB 7;	Length 348;
Best Local Similarity	77.8%;	Pred. No. 7.98e-86;		
Matches	235;	Conservative	0; Mismatches 64;	Indels 3; Gaps 3;
Db	50	tctgtgccaggtgcagctgcaggtagtcggccccaggactggtgaagccttcggagaacc	109	
Qy	47	TCTGTCTGATGTGCAGCTTCAGAGTTCGGGACCTGCTCGTGGAAGCCTTCATCATCTC	106	
Db	110	tgtccctcacctgcacatgtctcgttggttcccattcagtta-tac-tggagctgga	166	
Qy	107	TGTCCTCACCTGTACTGTCTGCTGCTACTCAATCCACAGTGATCATGCCGTGGAGGTGA	166	
Db	167	tccggcaagccccaaggaaaggaactggagtgattgggtatatctattacaatgggaagca	226	
Qy	167	TCCGGCAGTTTCCAGGAAACAAC TGAGTGGATGGGCTACATAA GTTACAGTGGTGATCA	226	
Db	227	ccaactcaaacccctccctcaagagtcgagtcaccatacatcagtagacagctccaagaacc	286	
Qy	227	CTACCTACACCCGATCTCTCAAAGTCCGATCTCTATCATCTCCAGACACATCCAAGACC	286	
Db	287	agttctccctgaagctgagctctgtgaccgttcggagacagcgctgtattactgtgcga	346	
Qy	287	AGTTCTTCTACAGTTGAATTCTGTGACTACTGGGACAGCTCCACATATTACTGTGCAA	346	
Db	347	ga 348		
Qy	347	Ga 348		

Search completed: Mon Jul 8 09:03:06 1996  
Job time : 42 secs.

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WATERMAN

(TM)

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MPsrch\_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 09:03:25 1996; MasPar time 190.43 Seconds

Tabular output not generated. 775.895 Million cell updates/sec

Title: >US-08-137-117B-30

Description: (1-411) from US08137117B.seq

Perfect Score: 411

N.A. Sequence: 1 ATCAGAGTCTGATTCCTTT.....CCTCAGTCACCGTCTCTCA 411

Comp: TACTCTCACCAGCTAAGAAA.....GGAGTCAGTGGCAGAGAGT

Scoring table:

TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

EST-STS  
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56  
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62  
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80  
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86  
87:EST87 88:EST88 89:STS1 90:STS2 91:STS3 92:STS4  
93:STS5 94:STS6

EST-STS-TWO

93:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5  
100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10  
105:gnEST11 106:gnEST12 107:gnEST13 108:gnEST14 109:gnEST15  
110:gnEST16 111:gnEST17 112:gnEST18 113:gnEST19 114:gnEST20  
115:gnEST21 116:gnEST22 117:gnEST23 118:gnEST24 119:gnEST25  
120:gnEST26 121:gnEST27 122:gnEST28 123:gnEST29  
124:gnEST30 125:gnEST31 126:gnEST32 127:gnEST33

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

Statistics: Mean 9.954; Variance 1.799; scale 5.535

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	137	33.3	478	16	H43753	yp21g01.r1 Homo sapie	1.01e-239
2	137	33.3	478	123	HS753236	yp21g01.r1 Homo sapie	1.01e-239
3	103	25.1	299	127	HST27727	EST13874 Homo sapiens	1.08e-164
4	103	25.1	299	69	T27727	EST13874 Homo sapiens	1.08e-164
5	100	24.3	410	13	H30111	yo59b04.r1 Homo sapie	3.57e-158
6	92	22.4	331	69	T27715	EST13381 Homo sapiens	6.72e-141
7	92	22.4	331	127	HST27715	EST13381 Homo sapiens	6.72e-141
8	73	17.8	234	69	T28164	EST30734 Homo sapiens	1.19e-100
9	73	17.8	234	127	HST28164	EST30734 Homo sapiens	1.19e-100
10	63	15.3	180	127	HST27730	EST13989 Homo sapiens	4.58e-80
11	63	15.3	180	69	T27730	EST13989 Homo sapiens	4.58e-80
12	57	13.9	169	47	R48619	y168a01.r1 Homo sapie	5.50e-68
13	41	10.0	367	78	T60021	yc01g07.r1 Homo sapie	3.12e-37
14	39	9.5	325	70	T29716	EST91759 Homo sapiens	1.36e-33
15	39	9.5	325	122	HS71611	EST91759 Homo sapiens	1.36e-33
16	38	9.2	253	70	T29661	EST89449 Homo sapiens	8.53e-32
17	38	9.2	253	122	HS66110	EST89449 Homo sapiens	8.53e-32
18	37	9.0	330	64	SSCID10	S.scrofa mRNA; expres	5.15e-30
19	37	9.0	330	129	SSCID10	S.scrofa mRNA; expres	5.15e-30
20	36	8.8	228	11	H24604	y140b06.r1 Homo sapie	2.99e-28
21	36	8.8	419	124	HS816226	ys11b01.r1 Homo sapie	2.99e-28
22	36	8.8	419	100	H73816	ys11b01.r1 Homo sapie	2.99e-28
23	34	8.3	422	125	HS952232	yo70g05.r1 Homo sapie	8.91e-25
24	34	8.3	422	16	H43952	yo70g05.r1 Homo sapie	8.91e-25
25	31	7.5	125	8	H15753	y127d09.r1 Homo sapie	1.02e-19
26	31	7.5	485	49	R54774	y175f04.r1 Homo sapie	1.02e-19
27	30	7.3	303	57	R83139	yp11g03.r1 Homo sapie	4.44e-18
28	29	7.1	446	53	R71741	y185d11.r1 Homo sapie	1.83e-16
29	26	6.3	147	16	H42647	yp13a12.r1 Homo sapie	8.57e-12
30	26	6.3	369	10	H22104	yl34f04.r1 Homo sapie	8.57e-12
31	26	6.3	418	78	T61697	yb86f08.r1 Homo sapie	8.57e-12
32	25	6.1	309	12	H27953	yl62c09.r1 Homo sapie	2.67e-10
33	25	6.1	412	12	H27044	yl65f02.r1 Homo sapie	2.67e-10
34	25	6.1	448	17	H46398	yp19d12.r1 Homo sapie	2.67e-10
35	24	5.8	48	16	H42610	yp13b04.r1 Homo sapie	7.62e-09
36	24	5.8	538	8	H16008	yl27b02.r1 Homo sapie	7.62e-09
37	23	5.6	189	89	DM68G85	D. melanogaster STS d	1.99e-07
38	23	5.6	223	121	HS593219	yu69e06.r1 Homo sapie	1.99e-07
39	23	5.6	223	99	H68593	yu69e06.r1 Homo sapie	1.99e-07
40	22	5.4	236	13	H33938	EST110390 Rattus sp.	4.70e-06
41	22	5.4	236	129	R39382	EST110390 Rattus sp.	4.70e-06
42	22	5.4	355	131	HS45ST35	Human Chromosome 4 (c	4.70e-06
43	22	5.4	355	93	HUM4ST35	Human Chromosome 4 (c	4.70e-06
44	21	5.1	329	10	H22208	yl38e08.r1 Homo sapie	9.97e-05
45	21	5.1	408	16	H42300	yo63g08.r1 Homo sapie	9.97e-05

## ALIGNMENTS

RESULT LOCUS	1	H43753	478 bp	mRNA	EST	31-JUL-1995
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Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: [tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org)  
For clone availability, additional sequence and expression  
information related to this EST, please contact the TIGR Database  
([tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org)).

NCBI gi: 609813	
FEATURES	Location/Qualifiers
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	/organism="Homo sapiens"
	/note="human"
	<1..>331
mrna	
BASE COUNT	62 a 90 c 91 g 80 t
ORIGIN	8 others

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Best Local Similarity 70.0%; Pred. No. 6,726-141;  
Matches 177; Conservative 0; Mismatches 73; Indels 3; Gaps 2;

Db	72	tctctgccagctgcagctgcagagtcgggcccaggaactggtgaagccttcggagacc	131
QY	47	TCCTGTCTCATGTGCAGCTTCAGGAGTCGGGACCTCTCTGTTGAAGCCTTCTCAGCTC	106
Db	132	tgctccctcaattgcaactgtctctgtgtgntcogtctacagtgacaattttnactggggct	191
QY	107	TGTCTCTCACCCTGCACCTGTCACTGGCTACTCAATCACCAGTCATCATG--C-CTGGAGCT	163
Db	192	gggtctccagcaggccccaggaagggtcgagtgagattgggactattttnatagtggga	251
QY	164	GGATCGCGCAGTTTCCAGGAAACAACTGGAGTGGTGGCTACATAGTTACAGTGGTA	223
Db	252	caactactactacaacngtccctcaggagtcagtgacccatttcctgtagcangtccagaa	311
QY	224	TCACTACCTAACCAACCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGA	283
Db	312	acaagttctccct	324
QY	284	ACCACTTCTCTCT	296

RESULT	7
ID	HST27715 standard; RNA; EST; 331 BP.
AC	T27715;
DT	12-JAN-1995 (Rel. 42, Created)
DT	07-SEP-1995 (Rel. 45, Last updated, Version 2)
DE	EST13381 Homo sapiens cDNA 5' end similar to immunoglobulin gamma
DE	heavy chain V region (CB:M37921) (HT:M3789).

Sci.	
OS	Homo sapiens (human)
OC	Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC	Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RN	[1]
RP	1-331
RA	Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
RA	Bult C.J., Lee N., Kirkness E.F., Weinstein K.G., Gocayne J.D.,
RA	White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
RA	Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.
RA	Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geophagen N.S.M.,
RA	Glocke A., Gnehm C.B., Hanna M.C., Hedblom E., Hinkle Jr P.S.,
RA	Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marrao S.M.,

RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,  
RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,  
RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,  
RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,  
RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,  
RA Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,  
RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,  
RA Weissner P.S., Olsen H., Raymond L., Wei Y.F., Wang J., Xu C.,  
RA Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,  
RA Baseltine W.A., Fields C., Fraser C.M., Venter J.C.;  
RT \*Initial Assessment of Human Gene Diversity and Expression  
RT Patterns Based Upon 52 Million Basepairs of cDNA Sequence\*;  
RL Unpublished.  
CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper  
CC Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:  
CC [tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org) For clone availability, additional sequence  
CC and expression information related to this EST, please contact the  
CC TIGR Database ([tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org)). NCBI gi: 609813  
FH KEY Location/Qualifiers

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1..331
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/note="human"
<1..>331
mRNA
Sequence 331 BP; 62 A; 90 C; 91 G; 80 T; 8 other;

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Query Match	22.4%	Score 92;	DB 127;	Length 331;
Best Local Similarity	70.0%;	Pred. No. 6.72e-141;		
Matches	177; Conservative	0; Mismatches	73; Indels	3; Gaps
				2;

D <b>b</b>	72	tctgtgccagcgtgcagcgtcgaggctgggcccgaagtcggtgaagccttcggagacc	131
Q <b>y</b>	47	TCTGTCTGATGCAGTTCAGGAGTCGGGACCTGCTCGTGGAAGCCTTCAGTCTC	106
D <b>b</b>	132	tgtccctcaacttgcactgctctgtgtgdtncgtctacagtgcacaattttnactggggct	191
Q <b>y</b>	107	TGTCCTCCATCGCATGTCACTGGCTACTCAATCACAGTGCATATG--C-CTGGAGCT	163
D <b>b</b>	192	gggtccgcgcagccccagagaaggcgtggagtgatgggaactatttttnatagtggga	251
Q <b>y</b>	164	GSATCGGGCGATTTCACGGAACAACAACTGSGAGTCGTGGCGCTACATAAGATTACAGTGGTA	223
D <b>b</b>	252	caaectactacaacngtccctcagggtcgtagtcacaatctccgtngacangtccagaa	311
Q <b>y</b>	224	TCACTACCTACAGAACCATCTCTCAAAGTCGAATCTCTATCACTCGAGACATCCAAGA	283
D <b>b</b>	312	acaagttctccct	324
Q <b>y</b>	284	ACCAAGTTCTTCT	296

8	RESULT	LOCUS	T28164	234 bp	mRNA	EST	06-SEP-1995
	DEFINITION	EST30734 Homo sapiens cDNA 5' end similar to immunoglobulin heavy chain V <sub>D</sub> J regions (GB:214206) (Ht:3118).					

Accession  
Number  
Keywords  
Source  
Organism  
EST.  
human primer=M13 Reverse library=Human Colon.  
Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 234)  
REFERENCE

## AUTHORS

Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Kline K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A., Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Meissner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C., Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M. and Venter J.C.

**TITLE**  
Initial Assessment of Human Gene Diversity and Expression Patterns  
Based Upon 52 Million Basepairs of cDNA Sequence  
Unpublished (1995)

## JOURNAL

## COMMENT

Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423

Email: [tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org)

For clone availability, additional sequence and expression  
information related to this EST, please contact the TIGR Database  
([tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org)).

NCBI gi: 610262

**FEATURES**  
source  
1..234  
Location/Qualifiers

/organism="Homo sapiens"  
/note="human"

mRNA  
<1..>234

BASE COUNT  
ORIGIN  
41 a 63 c 72 g 52 t 6 others

Query Match 17.8%; Score 73; DB 69; Length 234;

Best Local Similarity 74.3%; Pred. No. 1.19e-100;

Matches 104; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db 72 tctgtgtccaggtgcagctgcaggagtcgggncagagctgtgtacgttttngagacc 131

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Qy 47 TCCTGTCTGATGTCGACCTTCAGGAGTCGGACCTGCTCTGTGAGCCTTCTAGTCTC 106

Db 132 tgccttcacactgngctgtctgtgttactccataagaagtgttactactgggctgga 191

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Qy 107 TGTCCCTCACCTGCACGTGTCACTGGCTACTCAATCACCAGTGTATGCTGGAGCTGGA 166

Db 192 ttccggcagggccagggaac 211

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Qy 167 TCCGGCAGTTTCCAGGAAC 186

## RESULT

ID HST28164 standard; RNA; EST; 234 BP.

AC T28164;

DT 12-JAN-1995 (Rel. 42, Created)

DT 07-SEP-1995 (Rel. 45, Last updated, Version 2)

DE EST30734 Homo sapiens cDNA 5' end similar to immunoglobulin heavy

chain V, D, J regions (GB:214206) (HT:3118).

## KW

## EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.

## RP

## 1-234

RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

RA Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,

RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,

RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,

RA Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,

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RA Kelley J.M., Kline K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,

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RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,

RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,

RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,

RA Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,

RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,

RA Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,

RA Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,

RT \*Initial Assessment of Human Gene Diversity and Expression

Patterns Based Upon 52 Million Basepairs of cDNA Sequence\*;

RL Unpublished.

CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper

Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:

CC [tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org) For clone availability, additional sequence

and expression information related to this EST, please contact the

CC TIGR Database ([tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org)). NCBI gi: 610262

FH Key Location/Qualifiers

FT source 1..234

/organism="Homo sapiens"

/note="human"

FT mRNA <1..>234

FT SQ Sequence 234 BP; 41 A; 63 C; 72 G; 52 T; 6 other;

Query Match 17.8%; Score 73; DB 127; Length 234;

Best Local Similarity 74.3%; Pred. No. 1.19e-100;

Matches 104; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db 72 tctgtgtccaggtgcagctgcaggagtcgggncagagctgtgtacgttttngagacc 131

||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||

Qy 47 TCCTGTCTGATGTCGACCTTCAGGAGTCGGACCTGCTCTGTGAGCCTTCTAGTCTC 106

Db 132 tgccttcacactgngctgtctgtgttactccataagaagtgttactactgggctgga 191

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Qy 107 TGTCCCTCACCTGCACGTGTCACTGGCTACTCAATCACCAGTGTATGCTGGAGCTGGA 166

Db 192 ttccggcagggccagggaac 211

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Qy 167 TCCGGCAGTTTCCAGGAAC 186

## RESULT

10

ID HST27730 standard; RNA; EST; 180 BP.

AC T27730;

DT 12-JAN-1995 (Rel. 42, Created)

DT 07-SEP-1995 (Rel. 45, Last updated, Version 2)

DE EST13989 Homo sapiens cDNA 5' end similar to immunoglobulin heavy

chain, V region (GB:212364) (HT:3115).

## KW

## EST.

05 Homo sapiens (human)  
0C Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
0C Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea

RA	Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
RA	Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
RA	White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
RA	Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
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RA	Glocke A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,
RA	Kelley J.M., Klimke K.M., Kelley J.C., Liu L.I., Marmaros S.M.,
RA	Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
RA	Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
RA	Sauadek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
RA	Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
RA	Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrite A.,
RA	Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
RA	Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
RA	Weisner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
RA	Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
RA	Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;
RT	"Initial Assessment of Human Gene Diversity and Expression
RT	Patterns Based Upon 52 Million Basepairs of cDNA Sequence";
RL	Unpublished.

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

**KEYWORDS** EST.  
**SOURCE** human primer=M13 Reverse library=Human Synovial membrane.

Jul 8 08:56

US-08-137-117B-30.rst

17

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

## REFERENCE

## AUTHORS

Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,  
Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,  
White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W.,  
Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,  
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Merrick J.M., Moreno-Palancas R.F., McDonald L.A., Nguyen D.T.,  
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Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,  
Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,  
Coleman T.A., Collins E.-J., Dimke D., Feng P., Ferrie A.,  
Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M.,  
Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,  
Weissner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C.,  
Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,  
Hasseltine W.A., Fields C., Fraser C.M. and Venter J.C.

## TITLE

Initial Assessment of Human Gene Diversity and Expression Patterns

## JOURNAL

Based Upon 52 Million Basepairs of cDNA Sequence

Unpublished (1995)

Contact: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@db.tigr.org

For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database

(tdbinfo@db.tigr.org).

## FEATURES

source NCBI gi: 611814  
1..325 Location/Qualifiers  
/organism="Homo sapiens"  
/note="human"  
BASE COUNT 72 a 92 c 81 g 80 t  
ORIGIN

Query Match 9.5%; Score 39; DB 70; Length 325;

Best Local Similarity 75.3%; Pred. No. 1.36e-33;

Matches 58; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 88 ggtgtctctcacattacagctgcagcagctcaggtccaggtcgtggaagccctcgcag 147

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 43 GGTATCTGCTGTGATGTGGAGCTTCAGGAGTCGGGACCTGCTCTGTTGAAGCCCTTCAG 102

Db 148 accctctcactcaactg 164

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 103 TCTCTGCTCCCTCACCTG 119

## RESULT

15

ID HS71611 standard; RNA; EST; 325 BP.

AC T29716;

DT 09-JAN-1995 (Rel. 42, Created)

DT 08-SEP-1995 (Rel. 45, Last updated, Version 2)

Jul 8 08:56

US-08-137-117B-30.rst

18

DE EST91759 Homo sapiens cDNA 5' end similar to immunoglobulin heavy  
chain V<sub>D</sub>J regions (GB:M34029) (HT:3782).

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.

RN [1]

RP 1-325

RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

RA Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,

RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W.,

RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,

RA FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geohagen N.S.M.,

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RA Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M.,

RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,

RA Weissner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C.,

RA Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,

RA Hasseltine W.A., Fields C., Fraser C.M., Venter J.C.;

RA "Initial Assessment of Human Gene Diversity and Expression

Patterns Based Upon 52 Million Basepairs of cDNA Sequence";

RT Unpublished.

CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper

CC Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:

CC tdbinfo@db.tigr.org For clone availability, additional sequence

CC and expression information related to this EST, please contact the

CC TIGR Database (tdbinfo@db.tigr.org) . NCBI gi: 611814

EH Key Location/Qualifiers

FT source 1..325

FT /organism="Homo sapiens"

FT /note="human"

FT mRNA <1..>325

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Query Match 9.5%; Score 39; DB 122; Length 325;

Best Local Similarity 75.3%; Pred. No. 1.36e-33;

Matches 58; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 88 ggtgtctctcacattacagctgcagcagctcaggtccaggtcgtggaagccctcgcag 147

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Qy 43 GGTATCTGCTGTGATGTGGAGCTTCAGGAGTCGGGACCTGCTCTGTTGAAGCCCTTCAG 102

Db 148 accctctcactcaactg 164

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Qy 103 TCTCTGCTCCCTCACCTG 119

Search completed: Mon Jul 8 09:06:44 1996

Job time : 199 secs.

Jul 8 08:33

US-08-137-117B-24.mg

1

Jul 8 08:23

US-08-137-117B-24.mg

2

\*\*\*\*\*  
[Sequence alignment visualization showing gaps and matches between two sequences]  
\*\*\*\*\*

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MParch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Mon Jul 8 08:33:35 1996; MasPar time 33.32 Seconds  
Tabular output not generated. 784.272 Million cell updates/sec

Title: >US-08-137-117B-24  
Description: (1-393) from US08137117B.seq  
Perfect Score: 393  
N.A. Sequence: 1 ATGAGTGTGACACACTCTCT.....GGACCAAGCTGGAAATAAA 393  
Comp: TACCTCAGTCTGTGTGACGA.....CTGCTTCGACCTTATTTT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 84802 seqs, 33246950 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-geneseq22  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16

Statistics: Mean 8.287; Variance 5.196; scale 1.595

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	393	100.0	393	5	Q30753 p12-k2.	2.00e-242
2	344	87.5	417	16	Q90432 DNA encoding anti-idi	3.41e-209
3	331	84.2	438	16	Q90431 DNA encoding anti-idi	2.15e-200
4	303	77.1	396	14	Q83490 Mouse MAb 3B9 light c	1.81e-181
5	303	77.1	399	16	Q92501 Mouse antibody FB3-2	1.81e-181
6	299	76.1	723	16	Q92503 Mouse antibody F4-7	1.90e-179
7	297	75.6	336	16	Q98534 V1 coding sequence fr	2.03e-177
8	295	75.1	393	6	Q36609 Anti-CD4 antibody MT	4.53e-176
9	293	74.6	393	5	Q30757 p64-k4.	1.01e-174

10	290	73.8	330	16	Q90421 DNA encoding immunogl	1.07e-172
11	286	72.8	330	16	Q90422 Anti-encoding immunogl	5.31e-170
12	286	72.8	331	12	Q71394 Anti-carcinoembryonic	5.31e-170
13	295	72.5	393	6	Q34575 Antibody 4A2 light ch	2.51e-169
14	283	72.0	335	2	Q12683 Murine 1B4 light chai	5.59e-168
15	283	72.0	336	16	Q74148 Human thyroid stimula	5.59e-168
16	281	71.5	333	12	Q71286 Light chain variable	1.24e-166
17	279	71.0	451	1	Q04694 Light chain variable	2.77e-165
18	265	67.4	612	11	Q62631 Porphylin antibody li	7.34e-156
19	264	67.2	733	4	Q25658 Mouse 0.5beta anti-HI	3.46e-155
20	264	67.2	786	1	N90495 A V chi region gene.	3.46e-155
21	261	66.4	396	7	Q42987 Mouse 4C10 anti-idiot	3.60e-153
22	256	65.1	336	16	Q90420 DNA encoding immunogl	8.25e-150
23	256	65.1	354	16	Q90430 DNA encoding anti-idi	8.25e-150
24	256	65.1	1014	2	Q10834 Encodes kappa light c	8.25e-150
25	253	64.4	333	12	Q70372 Anti HIV antibody lig	8.54e-148
26	253	64.4	333	11	Q65554 Mouse anti-HIV mu5.5	8.54e-148
27	251	63.9	336	16	Q96285 Human IgE receptor-bi	1.88e-146
28	249	63.4	334	1	N90492 Gene fragment of immu	4.15e-145
29	249	63.4	900	1	Q04039 Anti-Leu 3a light cha	4.15e-145
30	247	62.8	333	14	Q82818 Murine NM-01 variable	9.12e-144
31	247	62.8	336	16	Q96283 Human IgE receptor-bi	9.12e-144
32	243	61.8	334	9	Q55002 Murine anti-CD18 Ab 6	4.14e-141
33	241	61.3	334	11	Q73749 Light chain variable	9.67e-140
34	240	61.1	336	2	Q10379 Chimeric MAb 9.2.27	1.45e-139
35	237	60.3	363	10	Q56688 Sequence of the monoc	4.65e-137
36	237	60.3	363	10	Q56686 Sequence of the monoc	4.65e-137
37	235	59.8	334	9	Q49617 Light chain variable	1.02e-135
38	235	59.8	336	2	Q12684 Murine 1B4 light chai	1.02e-135
39	235	59.8	363	6	Q37472 Sequence encoding the	1.02e-135
40	223	56.7	545	13	Q80292 Monoclonal antibody 2	1.10e-127
41	215	54.7	312	3	Q20309 B cell hybridoma 4:3.	2.45e-122
42	211	53.7	336	16	Q97506 Light chain variable	1.15e-119
43	201	51.1	309	10	Q55915 Light chain region of	5.36e-113
44	181	46.1	334	9	Q55000 Humanised anti-CD18 A	1.06e-99
45	167	42.5	393	14	Q73986 Humanized antibody 3B	1.98e-90

ALIGNMENTS

RESULT 1  
ID Q30753 standard; cDNA, 393 BP.  
AC Q30753;  
DT 30-MAR-1993 (first entry)  
DE p12-k2.  
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;  
KW plasmid; p12-k2; p12-h2; se.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT sig\_peptide 1..60  
FT /\*tag= a  
FT mat\_peptide 61..393  
FT /\*tag= b  
PN WO9219759-A.  
PD 12-NOV-1992.  
PF 24-APR-1992; J00544.  
PR 25-APR-1991; JP-095476.  
PR 19-FEB-1992; JP-032084.  
PA (CHUS ) CHUGAI SEIYAKU KK.  
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
DR WPI; 92-398882/48.  
PT Reconstituted human antibody to human interleukin-6 receptor -



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PT has low antigenicity and contains mouse V-region complementarity  
PT determining regions  
PS Disclosure; Page 118; 207pp; Japanese.  
CC The sequences given in Q30753-54 were used in example to illustrate  
CC the production of a human antibody which recognises human  
CC interleukin-6 receptor (IL-6R). The antibody comprises light (L)  
CC chain and heavy (H) chain variable regions which were derived from a  
CC mouse monoclonal antibody produced from the hybridoma AUK12-20 which  
CC contained the plasmids p12-k2 and p12-h2.  
SQ Sequence 393 BP; 98 A; 103 C; 103 G; 89 T;

Query Match 100.0%; Score 393; DB 5; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2,00e-242;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 atggagtcagacacactcctgctatgggtactgctgtctgggtccaggttccactggt 60  
|||||  
Qy 1 ATGGAGTCAGACACACTCTCTGTATGGGTACTGCTGCTTGGGTTCCAGGTTCCACTGGT 60  
|||||  
Db 61 gacattgtgtgacacagtcctcttcttcttaggtgtatctctggggcagaggccacc 120  
|||||  
Qy 61 GACATTGTGCTGACACAGTCTCTGCTTCTTAGGTGTATCTCTGGGCGAGAGGCCACC 120  
|||||  
Db 121 atctcatcagggccagcaaaagtgcagtacatctgcttatagttatgtcactgggtac 180  
|||||  
Qy 121 ATCTCATCGAGGGCCAGCAAAAGTGTCAGTACATCTGGCTATAGTTATATGCACTGGTAC 180  
|||||  
Db 181 caacagaaacccaggacagacacccccactcctcatctatcttgcacacactagaatct 240  
|||||  
Qy 181 CAACAGAAACCCAGGACAGACACCCAACTCCTCATCTATCTTGCATCCACCTAGAACT 240  
|||||  
Db 241 ggggtccctgccaggttcagtgccagtggtctgggacagacttccacctcaacatccat 300  
|||||  
Qy 241 GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300  
|||||  
Db 301 cctgtggaggaggaggtgctgcaacctattactgtcagcacagtagggaggaatccgtac 360  
|||||  
Qy 301 CCTGTGGAGGAGGAGGATGCTGCACCTTATCTGTCTCAGACAGTAGGAGGATCCGTAC 360  
|||||  
Db 361 acgttcggagggggaccaaagctggaataaaa 393  
|||||  
Qy 361 ACGTTGGAGGGGGGACCAAGCTGGAATAAAA 393  
|||||

RESULT 2  
ID Q90432 standard; DNA; 417 BP.  
AC Q90432;  
DT 02-FEB-1996 (first entry)  
DE DNA encoding anti-idiotypic antibody Idio20 clone 20KB1.  
KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;  
KW complementarity determining region; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 28..417  
FT /\*tag= a  
FT /product= anti-autoantibody\_Idio20  
FT sig\_peptide 28..90  
FT /\*tag= b  
PN J07101999-A.  
PD 18-APR-1995.  
PF 06-OCT-1993; 272950.  
PR 06-OCT-1993; JP-272950.  
PA (HAGI/) HAGIWARA Y.  
DR WPI; 95-182987/24.

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4

DR P-PSDB; R74967.  
PT Novel anti-idiotypic antibody against an human anticancer monoclonal  
PT antibody - and DNA sequences encoding the antibody, useful in  
PT pharmacology, medicine and biochemical fields.  
PS Example 5; Page 20; 28pp; Japanese.  
CC Q90425-Q90434 are DNA clones encoding anti-idiotypic antibodies  
CC Idio3, Idio17, Idio20, Idio27 and Idio33 against a human anticancer  
CC monoclonal antibody. These antibodies and DNA encoding them are useful  
CC in pharmacological, medical and biochemical fields of research.  
SQ Sequence 417 BP; 100 A; 110 C; 113 G; 94 T;

Query Match 87.5%; Score 344; DB 16; Length 417;  
Best Local Similarity 95.7%; Pred. No. 3.41e-209;  
Matches 376; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

Db 28 atggagacagacacactcctgctatgggtactgctgtctgggtccaggttccactggt 87  
|||||  
Qy 1 ATGGAGTCAGACACACTCTCTGTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGT 60  
|||||  
Db 88 gacattgtgtgacacagtcctcttcttcttaggtgtatctctggggcagaggccacc 147  
|||||  
Qy 61 GACATTGTGCTGACACAGTCTCTGCTTCTTAGGTGTATCTCTGGGCGAGAGGCCACC 120  
|||||  
Db 148 atctcatcagggccagcaaaagtgcagtacatctgcttatagttatgtcactgggtac 207  
|||||  
Qy 121 ATCTCATCGAGGGCCAGCAAAAGTGTCAGTACATCTGGCTATAGTTATATGCACTGGTAC 180  
|||||  
Db 208 caacagagacagagacagccaccagactcctcatctatcttgcacacactagaatct 267  
|||||  
Qy 181 CAACAGAAACCCAGGACAGACACCCAACTCCTCATCTATCTTGCATCCACCTAGAACT 240  
|||||  
Db 268 ggggtccctgccaggttcagtgccagtggtctgggacagacttccacctcaacatccat 327  
|||||  
Qy 241 GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300  
|||||  
Db 328 cctgtggaggaggaggtgctgcaacctattactgtcagcacagtagggaggaatccgtac 384  
|||||  
Qy 301 CCTGTGGAGGAGGAGGATGCTGCACCTTATCTGTCTCAGACAGTAGGAGGATCCGTAC 360  
|||||  
Db 385 acgttcggagggggaccaaagctggaataaaa 417  
|||||  
Qy 361 ACGTTGGAGGGGGGACCAAGCTGGAATAAAA 393  
|||||

RESULT 3  
ID Q90431 standard; DNA; 438 BP.  
AC Q90431;  
DT 02-FEB-1996 (first entry)  
DE DNA encoding anti-idiotypic antibody Idio17 clone 17KB1.  
KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;  
KW complementarity determining region; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 1..438  
FT /\*tag= a  
FT /product= anti-idiotypic\_antibody\_Idio17  
FT sig\_peptide 1..39  
FT /\*tag= b  
PN J07101999-A.  
PD 18-APR-1995.  
PF 06-OCT-1993; 272950.  
PR 06-OCT-1993; JP-272950.  
PA (HAGI/) HAGIWARA Y.  
DR WPI; 95-182987/24.

DR P-PSDB; RT4966.  
PT Novel anti-idiotypic antibody against a human anticancer monoclonal  
PT antibody - and DNA sequences encoding the antibody, useful in  
PT pharmacology, medicine and biochemical fields.  
PS Example 5; Page 19; 28pp; Japanese.  
CC Q90425-Q90434 are DNA molecules encoding anti-idiotypic antibodies  
CC Id3o3, Id3o17, Id3o20, Id3o27 and Id3o33 against a human anticancer  
CC monoclonal antibody. These antibodies and DNA encoding them are useful  
CC in pharmacological, medical and biochemical fields of research.  
SQ Sequence 438 BP; 104 A; 120 C; 112 G; 102 T;

Query Match 84.2%; Score 331; DB 16; Length 438;  
Best Local Similarity 96.5%; Pred. No. 2.15e-200;  
Matches 359; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

1	ctatgggtactgctgctctgggttccagggttccactggtgacattgctgtgacacagtcct	60
22	ctatgggtactgctgctctgggttccagggttccactggtgacattgctgtgacacagtcct	81
Qy		
61	ctctgttctttagctgtatctctgggagaggcctccatctcatcacagggccagcaaa	120
Db		
82	ctgtgttctttagctgtatctctgggagaggcctccatctcatctgcagggcgacgaaa	141
Qy		
121	agtgcagtcacatctggctatagttatatgcactggaaacaaagaaacaggacagcca	180
Db		
142	asgtgcagtcacatctggctatagttatatgcactgggtaccacagaaacaggacagcca	201
Qy		
181	cccagactctcatctatcttgtatccaaactagaatctggggctccctgccaggttcagt	240
Db		
202	cccaaaactcctcatctatcttgcatccaacctagaaatctgggggtccctgccaggttcagt	261
Qy		
241	ggcagtggtgtctgggacagacttcaacctcaacatccatctgtggaggaggagatgct	300
Db		
262	ggcagtggtgtctgggacagacttcaacctcaacatccatctgtggaggaggagatgct	321
Qy		
301	gcaacctattactgtcagcacattagg--gag---cttcacgcttcggagggggaccaaag	357
Db		
322	gcnaacttattactgtcagcacattaggagaaatccgtacacgcttcggagggggaccaaag	381
Qy		
358	ctggaaataaaaa	369
Db		
382	ctggaaataaaaa	393
Qy		

RESULT 4

ID	Q83490 standard; cDNA; 396 bp.
AC	Q83490;
DT	20-SEP-1995 (first entry)
DE	Mouse MAB 389 light chain.
KW	Chimeric antibody; humanized antibody; antibody engineering;
KW	monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.

Location/Qualifiers	1..396
---------------------	--------

FT	/*tag= a	
FT	sig_peptide	1..60
FT	/*tag= b	
FT	mat_peptide	61..396
FT	/*tag= c	
PN	W09507301-A.	
PD	16-MAR-1995.	
PF	07-SEP-1994;	U10308.
PF	07-SEP-1993;	US-117366.
PR	14-OCT-1993;	US-136783.

PA	(SMIK ) SMITHKLINE BEECHAM CORP.
PA	(SMIK ) SMITHKLINE BEECHAM PLC.
PI	Gross MS, Holmes SD, Sylvester DR;
DR	WPI; 95-123387/16.
DR	P-PSDB; R70189.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT	from high affinity mAbs - useful in treatment of IL-4-mediated
PT	and IgE-mediated allergic conditions
PS	Disclosure; Fig.1; 97pp; English.
CC	Spleen cells from mice immunized with human IL-4 were used to prepare
CC	hybridomas, which were screened for anti-IL-4 MAb secretion. Only
CC	clone 3B9 was positive.
CC	chains were cloned into pGEM7f+ and transformed into E. coli
CC	DH5-alpha. The clones were sequenced (Q83490-91), and used for
CC	antibody engineering.
SQ	Sequence 396 bp; 99 A; 103 C; 91 T;

```
Query Match      77.1%; Score 303; DB 14; Length 396;
Best Local Similarity 88.5%; Pred. No. 1.81e-181;
Matches 348; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
```

Db	1	atggagacagacacaatcctgctatgggtgtgctgctctgggttccagggtccactgggt	60
Qy	1	ATGGAGTCAAGACACACTCTCTGCTATGGGTACTGCTGCTCTGGGTTCAGGTTCCACTGGT	60
Db	61	gacattgtgtgacccaatctccagctcttttggctgtgtctctagggcagagggccacc	120
Qy	61	GACATTGTGCTGACACAGTCTCTGCTCTCTTACGGTGTATCTCTGGGGCAGAGGGCCACC	120
Db	121	atctctgcgaaggccagccaagtgttgattatgatggtagtgattatatgaactgggtac	180
Qy	121	ATCTCATGCGGGCCAGGAAAGTGCAGTACACTCTGGCTAGTATTATGCACTGGGTAC	180
Db	181	caacagaacaggagacagcaccaccaactctcatctatgtgcatccaatcagaatct	240
Qy	181	CAACAGAAACAGGACAGACAGACCACAAACTCCTTCATCTATCTTTGCATCCAACTAGAAATCT	240
Db	241	gggatccagccaggtttagtggcagtggtctgggacagactcaccctcaacatccat	300
Qy	241	GGGATCCCTCGCCAGTTTCACTGGCAGTGGGCTCTGGGACAGACTTCACCTCAACATCGAT	300
Db	301	ccctggaggagagagatgcgaacctattactgcacgaagttaatgagatccctccg	360
Qy	301	CCTCTGGAGGAGGAGGATGCTCGAACTTACTCTCAGCACAGTAGGGAGAATCCGTAC	360
Db	361	acgttcggtggaggcaccacgctggaaatcaaa	393
Qy	361	ACGTTCCGAGGGGGGACCAGCTGGAAATAAAA	393

RESULT	5
ID	Q92501 standard; cDNA; 399 BP.
AC	Q92501;
DT	07-FEB-1996 (first entry)
DE	Mouse antibody FB3-2 light chain variable region coding sequence.
KW	Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
KW	antibody; immunotolerance; animal; variegated display library;
KW	variable region; antigen; immunorecessive; cell surface marker; foetal;
KW	cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
KW	familial hypercholesterolaemia; binding affinity; ds.
OS	Mus musculus.
FH	Key
FT	CDS Location/Qualifiers
FT	*tag= a 67..399

FT /product= antibody FB3-2 light chain variable region  
PN W09515982-A2.  
PD 15-JUN-1995.  
PP 08-DEC-1994; U14106.  
PR 08-DEC-1993; US-164022.  
PR 06-DEC-1994; US-350400.  
PA (GENZ ) GENZYME CORP.  
PI Barsonian G, Copeland DP, Hillhouse D, Johnson T;  
DR WPI; 95-224291/29.  
DR P-PSDB; R75457.  
PT Generating new antibodies specific for immunorecessive epitopes -  
PT by selection from variegated V gene library cloned from  
PT immuno:tolerance derived antibody repertoire, useful in diagnosis,  
PT purificn. and therapy, e.g. of cancer  
PS Disclosure; page 76-77; 109pp; 109pp; 109pp.  
CC The coding sequence of the light chain variable region from the mouse  
CC antibody FB3-2. This sequence was isolated from a variegated display  
CC library (VDL) of variable regions derived from a repertoire of antibodies  
CC from an immunotolerised animal. The VDL is generated by PCR amplifying  
CC the variable regions from the antibody coding sequences using the primers  
CC Q74153-74. The variable regions, esp the complementarity determining  
CC regions (CDR; see R75462-93 for examples of CDRs) from the immunotolerant  
CC animals' antibodies are used to construct an antibody against a  
CC immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or  
CC stem cell, which can differentiate between variant or related forms of  
CC the antigen. The antibodies generated can be used in the diagnosis, e.g.  
CC detection of the immunorecessive antigen, or in therapy e.g. of cancer,  
CC Alzheimer's disease or familial hypercholesterolaemia. The method of  
CC production of the antibody allows rapid and sensitive isolation of  
CC antibodies that would be difficult to isolate by standard methods. The  
CC antibodies produced have greater binding affinity than those produced by  
CC combinatorial/hybridoma methods.  
SQ Sequence 399 BP; 105 A; 99 G; 86 T;

Query Match 77.1%; Score 303; DB 16; Length 399;  
Best Local Similarity 95.5%; Pred. No. 1.81e-181;  
Matches 318; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

**Db** 67 gacattgtgatgaccagctcctccttcccttagctgtatctctggggcgagggccacc 126  
||||||| ||| |  
**Ov** 61 GACATTCTGTCACAGACTCCCTGCTTCTTAGTGTA TCTCTGGGGCAGGGGCACC 120  
||||||| ||| |

Db 127 atctcatgcaggccagccaaagtgtcagtagacatctagatatagttatatgcactagtac 186  
|||||  
Ov 121 ATCTCATGCGGGCCAGCAAAGTGTCACTACATCTGGCTATAGTTTATATGCACTGGTAC 180

Db 187 caacagaaacacgagcagccgcaactcctcatcaagtttgatcccaactagaatct 246  
|||||  
Ov 181 caacagaaacacgagcagaccacccactcctcatctatcttcgacccacactagaatct 240  
|||||

Db 247 ggggtccctgccaggttcagtggcagtggtgtggacagacttcacctcaacatccat 306  
|||||  
Qw 241 ggggtccctgccaggttcagtggcagtggtgtggacagacttcacctcaacatccat 300  
|||||

Db 307 cctgtggaggaggaatactgcaacataattactgtcagcacagttgggagattccgtac 366  
|||||  
301 cctgtggaggaggaatactgcaacataattactgtcagcacagttgggagattccgtac 360  
|||||

Db 367 acgttcggaggggggaccaaactggaataaaa 399  
|||||  
|||

## RESULT 6

ID	Q92503 standard; cDNA; 723 BP.	
AC	Q92503;	
DT	07-FEB-1996 (first entry)	
DE	Mouse antibody F4-7 light chain variable region coding sequence.	
KW	Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;	
KW	antibody; immunotolerance; animal; variegated display library;	
KW	variable region; antigen; immunorecessive; cell surface marker; foetal;	
KW	cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;	
KW	familial hypercholesterolaemia; binding affinity; ds.	
OS	Mouse musculus.	
FT	Key	Location/Qualifiers
FT	CDS	67..399
FT	/*tag= a	
FT	/product= antibody F4-7 light chain variable region	
PN	W09515982-A2.	
PD	15-JUN-1995.	
PD	08-DEC-1994; U14106.	
PR	08-DEC-1993; US-164022.	
PR	06-DEC-1994; US-350400.	
PA	(GENZ ) GENZYME CORP.	
PI	Barsonian G, Copeland DP, Hillhouse D, Johnson T;	
DR	WPI; 95-224291/29.	
DR	P-PSDB; R75459.	
PT	Generating new antibodies specific for immunorecessive epitopes -	
PT	by selection from variegated V gene library cloned from	
PT	immunotolerance derived antibody repertoire, useful in diagnosis,	
PT	purificn. and therapy. e.g. of cancer	
PS	Disclosure; Page 80-81; 109pp; English.	
CC	The coding sequence of the light chain variable region from the mouse	
CC	antibody F4-7. This sequence was isolated from a variegated display	
CC	library (VDL) of variable regions derived from a repertoire of antibodies	
CC	from an immunotolerised animal. The VDL is generated by PCR amplifying	
CC	the variable regions from the antibody coding sequences using the primers	
CC	Q74153-74. The variable regions, esp the complementarity determining	
CC	regions (CDR; see R75462-93 for examples of CDRs) from the immunotolerant	
CC	animals' antibodies are used to construct an antibody against a	
CC	immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or	
CC	stem cell, which can differentiate between variant or related forms of	
CC	the antigen. The antibodies generated can be used in the diagnosis, e.g.	
CC	detection of the immunorecessive antigen, or in therapy e.g. of cancer,	
CC	Alzheimer's disease or familial hypercholesterolaemia. The method of	
CC	production of the antibody allows rapid and sensitive isolation of	
CC	antibodies that would be difficult to isolate by standard methods. The	
CC	antibodies produced have greater binding affinity than those produced by	
CC	combinatorial/hybridoma methods.	
SQ	Sequence 723 BP; 205 A; 195 C; 172 G; 151 T;	

Query Match	76.1%	Score 299;	DB 16;	Length 723;
Best Local Similarity	94.9%;	Pred. No. 9.06e-179;		
Matches	316;	Conservative	0;	Mismatches 17;
		Indels	0;	Gaps 0;

**Db** 67 gacattgtgatgaccagtcctccttcccttagcttgatctctgggcagaggcccac 126  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
**Ov** 61 GACATTTCGTCACACAGTCTCCCTGCTCCCTTAGCTGTATCTCTGGGCACAGGCCACC 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

**Db** 127 atctcatgcagggtcaggaagtgtcagtagacatctagccatatggttatgtcactgggtac 186  
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**Gv** 121 arctcatgcagggcccaccacaagaattctcacatcaatccccatactattatgccacttccctac 180  
|||||

Db 187 caacagaaaccagacagccaccccaactctcatcaagtatgcatccaactagaatct 246

Db 247 ggggtccctgccaggttcagtggcagtgggtctgggacagacttcacctcaacatccat 306

## RESULT 6

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9

Qy 241 GGGGTCCCTCCGAGGTTGAGTGGAGTGGGTCTGGGACAGACTTCACCTGCACATCCAT 300  
Db 307 cgtgtgagagagagatactgcaacataattactgtcagcacagttggagattccgtac 366  
Qy 301 CTGTGGAGGAGGAGTGTGTCACACTATTACTGTGACACAGTAGGAGAAATCCGTAC 360  
Db 367 acgttcagaggggggaccaaagctggaataaaa 399  
Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAAATAAAA 393

RESULT 7

ID Q98534 standard; DNA; 336 BP.  
AC Q98534;  
DT 27-FEB-1996 (first entry)  
DE V1 coding sequence from an antibody against cancer-specific mucin.  
KW Antibody; heavy chain; light chain; variable region; cancer; mucin;  
KW hybridoma cell; murine; mouse; pancreatic cancer cell; expression vector;  
KW Fv; human; constant domain; chimera; anaphylaxis; ss.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT misc\_feature 70..114  
FT /\*tag= a  
FT /note= "encodes CDR1"  
FT misc\_feature 160..180  
FT /\*tag= b  
FT /note= "encodes CDR2"  
FT misc\_difference 190..192  
FT /\*tag= c  
FT /transl\_except= seq; GAG a.a.: Asp  
FT misc\_feature 277..303  
FT /\*tag= d  
FT /note= "encodes CDR3"  
PN FR2714915-A1.  
PD 13-JUL-1995.  
PF 13-JAN-1995; 000349.  
PR 13-JAN-1994; JP-002131.  
PA (TOYO ) TOSOH CORP.  
PI Chung Y, Iba Y, Kaneko T, Sowa M, Yasukawa K;  
DR WP1; 95-247908/33.  
DR P-PSDB; R80272.  
PT New variable domains of antibody recognising cancer specific mucin  
PT - and related DNA and expression vectors, producing chimeric  
PT mouse-human antibody for diagnosis and treatment of cancer  
PS Claim 8; Page 16-17; 25pp; French.  
CC The nucleotide sequence of the variable region from the light chain of an  
CC antibody against cancer-specific mucin. The coding sequence was isolated  
CC from N2 hybridoma cells expressing a murine antibody reactive with  
CC pancreatic cancer cells. The DNA encoding the antibody variable regions  
CC from the heavy (Q98533) and light chains were isolated and inserted into  
CC vectors. These vectors express the domains as an Fv antibody. Vectors  
CC which additionally contain genes encoding the human constant domains  
CC express a chimeric mouse-human antibody. The antibodies are useful in  
CC the detection and treatment of cancer. The chimeras should be less likely  
CC to cause anaphylaxis than the original murine antibody.  
SQ Sequence 336 BP; 83 A; 92 C; 84 G; 77 T;

Query Match 75.6%; Score 297; DB 16; Length 336;  
Best Local Similarity 94.6%; Pred. No. 2.03e-177;  
Matches 315; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 1 gacattgtctgacagactctccttcttagctgtatctgtggcgagagggccacc 60  
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10

Qy 61 GACATTGCTGCACACAGTCTCTGCTTCTTAGGTGTATCTCTGGGCGAGAGGCCACC 120  
Db 61 atctcatgagggccagcaaaagtgtcactacatctgactttagttatgtcaactgggtac 120  
Qy 121 ATCTCATGCGAGGGCCGCAAAAGTGTGATGATCTGGCTATAGTATTATGCACTGGTAC 180  
Db 121 caacagaaacccggagcagccaccacaaactcctcctctatctgtgacctcaaacctagaact 180  
Qy 181 CAACAGAAACCCAGGACAGACACCCAAACTCCTCATCTATGCTTGCATCCAACTAGAACT 240  
Db 181 ggggtccctgagaggttcagtgagcagtggggtctgggacagacttcacctcaaacatccat 240  
Qy 241 GGGGTCCCTCCAGGTTGAGTGGCATGGGTCTGGGACAGCTTCACCTCAACATCCAT 300  
Db 241 cctgtggagagaggagtgctgcaacctattactgtcagcagtagggaggttccgtgg 300  
Qy 301 CTGTGCGAGGAGGATGCTGCACCTATTACTGTGACACAGTAGGGAGAAATCCGTAC 360  
Db 301 acgttcgtgtgagggaccacaaactggaataaaa 333  
Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAAATAAAA 393

RESULT 8

ID Q36609 standard; DNA; 393 BP.  
AC Q36609;  
DT 02-JUN-1993 (first entry)  
DE Anti-CD4 antibody MT 3.10 light chain variable region.  
KW immunosuppression; tissue transplantation; graft; L chain; V region;  
KW T-helper cell inhibition; transplant rejection; Mab;  
KW Interleukin-2 receptor; ss.  
FH Key Location/Qualifiers  
FT sig\_peptide 1..60  
FT /\*tag= a  
FT mat\_peptide 61..393  
FT /\*tag= b  
FT /note= "V1 region begins at position 361"  
PN DE4143214-A.  
PD 28-JAN-1993.  
PF 30-DEC-1991; 143214.  
PR 25-JUL-1991; DE-124759.  
PR 30-DEC-1991; DE-143214.  
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
PI Kaluza B, Rietmueller G, Scheuer W, Weidle U;  
DR WP1; 93-037582/05.  
DR P-PSDB; R32123.  
PT Synergistic antibody compsn. for use as immunosuppressant -  
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
PT alpha- or anti-IL2R beta antibodies  
PS Claim 5; Page 11; 18pp; German.  
CC This sequence encodes the light chain variable region of a preferred  
CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
CC composition. Mab MT 3.10 is deposited as clone 3.101/sB10 (ECACC  
CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R  
CC alpha or beta antibody. Individually the antibodies are strongly  
CC inhibiting and when used together their immunosuppressive properties  
CC are improved; they synergistically inhibit T-helper cell  
CC proliferation to effectively inhibit transplant rejection at low  
CC doses without significantly reducing the general immune response.  
CC See Q36607-Q36616.  
SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;

Query Match 75.1%; Score 295; DB 6; Length 393;  
Best Local Similarity 87.5%; Pred. No. 4.53e-176;









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Db 121 caacagaaccagagcagaccacccagactctcatctatcttctgtatccaaacctagaatct 180  
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Qy 181 CAACAGAAACAGGACAGACACCAAACTCCTCATCTATCTTGCATCCAACTAGAACTCT 240  
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Db 181 ggggtccctgccaggttcagtgccagtggtctaggacagacttcacccctcaacatccat 240  
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Qy 241 GGGGTCCCTGCCAGGTTTCAGTGGCAGTGGTCTGGGACAGACTTCACCTCAACATCCAT 300  
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Db 241 cctgtggaggaggatgtgcaacctattactgtcagcacattaggagc-t---tac 296  
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Qy 301 CCTGTGAGGAGGAGGATGCTGCACTTACTGTGACGACAGTAGGAGGATCCGTAC 360  
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Db 297 acgttcgaggggggacccaagctggaaataaaa 329  
|||||  
Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAAATAAAA 393  
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## RESULT 15

ID Q74148 standard; DNA; 336 BP.  
AC Q74148;  
DT 01-FEB-1996 (first entry)  
DE Human thyroid stimulating hormone antibody light chain variable region.  
KW thyroïd stimulating hormone; TSH; human; variable region; light;  
KW chain; antibody; chimeric antibody; *se*.  
OS Homo sapiens.  
PN J07132097-A.  
PD 23-MAY-1995.  
PF 28-JUN-1993; 156707.  
PR 28-JUN-1993; JP-156707.  
PA (TOYJ ) TOSOH CORP.  
DR WPI; 95-220118/29.  
PT DNA encoding an antibody recognising human thyroid-stimulating  
PT hormone - and preparation of chimeric antibody by expressing the  
PT DNA in a transformed host cell  
PS Claim 8; Fig 4; 8pp; Japanese.  
CC The DNA encodes the light chain variable region of an antibody  
CC recognising human thyroid stimulating hormone (hTSH). Prepn. of a  
CC chimeric antibody by expressing the DNA in a transformed host cell  
CC is also claimed. The anti-hTSH antibody has an additional useful  
CC function which could not be given by a mouse derived anti-TSH monoclonal  
CC antibody (*se*).  
SQ Sequence 336 BP; 85 A; 94 C; 81 G; 76 T;

Query Match 72.0%; Score 283; DB 16; Length 336;  
Best Local Similarity 92.5%; Pred. No. 5.59e-168;  
Matches 308; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 61 GACATTGTGTGACACAGCTCTCTGCTTCCTTAGGTGTATCTCTGGGGCAGAGGGCCACC 120  
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Db 61 atctcatgaggggcagcagagtgctcagttcatctagctatagttatgtcactggttac 120  
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Qy 121 ATCTCATCGGGCCAGCAGAAAGTGTCAGTAGATCTGGCTATAGTTATGCACTGGTAC 180  
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Db 121 caacagaaccagcagaccacccaactcctcatcaagtttgcatccaacctagaatct 180  
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Qy 181 CAACAGAAACAGGACAGACACCAAACTCCTCATCTATCTTGCATCCAACTAGAACTCT 240  
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Db 181 ggggtccctgccaggttcagtgccagtggtctggagacagacttcacccctcaacatccat 240  
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Qy 241 GGGGTCCCTGCCAGGTTTCAGTGGCAGTGGTCTGGGACAGACTTCACCTCAACATCCAT 300  
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Db 241 cctgtggaggagcagatgctgcaacatattactgtcaacacacttggagattcctcgg 300  
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Db 301 acgttcggtggaggcaccacgaagctggaaataaaa 333  
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Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAAATAAAA 393  
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Search completed: Mon Jul 8 08:34:22 1996  
Job time : 47 secs.

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and is derived by analysis of the total score distribution.

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3

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REFERENCE 1 (bases 1 to 393)
AUTHORS Jeffrey,P.D., Schildbach,J.F., Chang,C.Y., Kussie,P.H., Sheriff,S.
          and Margolies,M.N.
TITLE Structure and specificity of the anti-digoxin antibody 40-50
JOURNAL Unpublished (1994)
COMMENT NCBI gi: 476719
FEATURES
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        location/Qualifiers
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                /organism="Mus musculus"
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        Best Local Similarity 95.2%; Pred. No. 0.00e+00;
        Matches 374; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 1 atggagacagacacactcgttatggtagctgctcgtcgggtccaggtccactggt 60
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Db 61 gacattgtgtgacacagtcctcgttcctcgttcctcgttcctcgttcctcgttc 120
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Qy 61 GACATTGTGTGACACACTCCTGCTGCTTCCTTAGGTGTATCTCTGGGCGACAGGCGCACC 120

Db 121 atctcatcagggccagcaaaagtgtcagtcacatctgggtctatgctacatcattac 180
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Db 361 acgttcggtgctgggaccgagctggagctgaaa 393
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RESULT 2
ID MMIGKV386 standard; RNA; ROD; 390 BP.
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AC X91670;
DT 29-SEP-1995 (Rel. 45, Created)
DE M.musculus mRNA for Ig kappa light chain variable region (cell line
DE 3B6)
KW complementarity determining region; immunoglobulin variable region;
KW kappa light chain.
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RA Carceller A., Rosell-Vives E., Gomez-Roig A., Adan J., Sproll M.,
RA Piulats J.;
RT "Immunological and structural properties of anti-idiotypic
RT antibodies mimicking an epitope of human epidermal growth factor
RT receptor.";
RL Unpublished.
RW [2]
RP 1-390
RA Rosell-Vives E.;
RT ;
RL Submitted (19-SEP-1995) to the EMBL/GenBank/DBJ databases.
RL E. Rosell-Vives, MERCK, Farma y Quimica S.A., Caspe 108, E-08010
RL Barcelona, SPAIN
FH Key Location/Qualifiers
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    /cell_line="3B6"
    /chromosome="6"
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    1..>390
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    /note="pid:e200732"
    1..390
    V_region
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        130..174
        /note="complementarity-determining region 1"
        225..240
        /product="CDR2"
        /note="complementarity-determining region 2"
        340..360
        /product="CDR3"
        /note="complementarity-determining region 3"
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Query Match 89.1%; Score 350; DB 14; Length 390;
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Matches 379; Conservative 0; Mismatches 11; Indels 3; Gaps 2;

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Qy 1 ATGGAGTCAGACACACTCCTGCTATGGGTACTGCTGCTGGGTTCCAGGTTCCACTGCT 60

Db 61 gacattgtgtgacacagtcctcgttcctcgttcctcgttcctcgttcctcgttc 120
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RESULT 2
ID MMIGKV386 standard; RNA; ROD; 390 BP.
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5

Db 121 atctcatcagggccagcagaaagtgcagtacatctggctatagttatgtatgcaciggaac 180  
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Db 358 acgttcggagggggaccagctggaataaaaa 390  
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Qy 361 AC GTTCGGAGGGGACCAAGCTGGAAATAAAA 393

RESULT 3  
LOCUS MMIGKV386 390 bp RNA ROD 24-OCT-1995  
DEFINITION M.musculus mRNA for Ig kappa light chain variable region (cell line 386).  
ACCESSION X91670  
KEYWORDS complementarity determining region; immunoglobulin variable region; kappa light chain.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 390)  
AUTHORS Carceller,A., Rosell-Vives,E., Gomez-Roig,A., Adan,J., Sproll,M., and Pluats,J.  
TITLE Immunological and structural properties of anti-idiotypic antibodies mimicking an epitope of human epidermal growth factor receptor  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 390)  
AUTHORS Rosell-Vives,E.  
TITLE Direct Submission  
JOURNAL Submitted (19-SEP-1995) to the EMBL/GenBank/DBJ databases. E. Rosell-Vives, MERCK, Farma y Quimica S.A., Caspe 108, E-08010 Barcelona, SPAIN  
COMMENT NCBI gi: 1001882  
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6

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Qy 301 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTACGACAGTAGGGAGAAATCCGTAC 360

RESULT 4  
LOCUS MMIGKV 429 bp RNA ROD 04-AUG-1992  
DEFINITION Mouse mRNA for nonfunctionally rearranged Ig-kappa V/Jk2 region.  
ACCESSION X05184 M31709  
KEYWORDS Ig kappa light chain; Ig light chain.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 429)  
AUTHORS Strohal,R., Kroemer,G., Wick,G. and Kofler,R.  
TITLE Complete variable region sequence of a nonfunctionally rearranged

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kappa light chain transcribed in the nonsecretor P3-X63-Ag8.653 myeloma cell line  
 JOURNAL Nucleic Acids Res. 15 (6), 2771 (1987)  
 MEDLINE 87174798  
 COMMENT The nonfunctional transcript shows 98% homology to the Balb/c Vk21-E germline gene.  
 Data kindly reviewed (18-May-1988) by Strohal R.

NCBI gi: 52542  
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 41..100 /note="leader peptide (AA -20 to -1)"  
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 Matches 379; Conservative 0; Mismatches 10; Indels 4; Gaps 2;  
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 Db 101 gacattgtgctgacacagctcctgcttcccttagctgtatctctgggagagggccacc 160  
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 Db 161 atctcaccagggcagacaaagtcagtcacatctggctatagttatgactggaac 220  
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 Db 281 ggggtccctgccagggttcagtgccagtggtgctggagacagactcaccctcaacatccat 340  
 Qy 241 GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCCATCCAT 300  
 Db 341 cctgtggagagagagagtgctgcaacctattactgtcagacattaggagc-t---tac 396  
 Qy 301 CCTGTGGAGGAGGAGTCTGCAACCTATTACTGTTCAGACAGACTAGGGAGATCCGTAC 360  
 Db 397 acgttcgaggggggacccaagctggaataaaa 429  
 Qy 361 ACCTTCGGAGGGGGGACCAACCTGGAATAAAA 393

RESULT 5  
 LOCUS MUS1GKCSU 444 bp mRNA ROD 12-JUN-1993  
 DEFINITION Mouse Ig aberrantly rearranged kappa-chain mRNA V-J2-C-region, complete cds.  
 ACCESSION M35669  
 KEYWORDS C-region; J-region; V-region; immunoglobulin light chain;

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8

immunoglobulin-kappa.  
 SOURCE Mouse myeloma MOPC-21, cDNA to mRNA.  
 ORGANISM Mus musculus  
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
 Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
 REFERENCE 1 (bases 1 to 444)  
 AUTHORS Carroll, W.L., Mendel, E. and Levy, S.  
 TITLE Hybridoma fusion cell lines contain an aberrant kappa transcript  
 JOURNAL Mol. Immunol. 25, 991-995 (1988)  
 MEDLINE 89112230  
 COMMENT NCBI gi: 197295

FEATURES  
 source Location/Qualifiers  
 1..444 /organism="Mus musculus"  
 sig\_peptide 28..87 /note="Ig kappa-chain V-J2-C-region signal peptide"  
 /codon\_start=1  
 CDS 28..414 /note="Ig kappa-chain V-J2-C-region precursor; NCBI gi: 309369"  
 /codon\_start=1  
 mat\_peptide 88..411 /note="Ig kappa-chain V-J2-C-region"  
 /translation="METDTLLLVLLWPGTGDIVLTQSPASLAVSLQRATISYR  
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 EEEDAATYYCQHIRELTRSEGGSWK"  
 BASE COUNT 108 a 122 c 111 g 103 t  
 ORIGIN Chromosome 6.

Query Match 87.8%; Score 345; DB 56; Length 444;  
 Best Local Similarity 96.4%; Pred. No. 0.00e+00;  
 Matches 379; Conservative 0; Mismatches 10; Indels 4; Gaps 2;  
 Db 28 atgagacagacacactcctgttgggtactgctgctggttccagggtccactggt 87  
 Qy 1 ATGGAGTCAGACACACTCCTGCTATGGGTACTGCTGCTGGGTTCAGGTTCCACTGGT 60  
 Db 88 gacattgtgctgacacagctcctgcttcccttagctgtatctctgggagagggccacc 147  
 Qy 61 GACATTGTGTCAGACAGCTCCTGCTTCCCTTAGGTGTATCTCTGGGTCAGAGGGCCACC 120  
 Db 148 atctcaccagggcagccaaagtgcagtcacatctggtatagttatgcaactggaac 207  
 Qy 121 ATCTCATCGAGGGCCAGCAAAAGTGTGCATCATCTGGCTATAGTTATATGCATGGTAC 180  
 Db 208 caacagaaccaggacagccaccagactcctcatctatctgtatccaaacctagaatct 267  
 Qy 181 CAACAGAACCCAGGACAGACACCCAACTCCTCATCTATCTTGCATCCAACTAGATCT 240  
 Db 268 ggggtccctgccagggttcagtgccagtggtgctgggagacagactcaccctcaacatccat 327  
 Qy 241 GGGGTCCCTGCCAGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCCATCCAT 300  
 Db 328 cctgtgagagagagagtgctgcaacctattactgtcagcattaggagc-t---tac 383  
 Qy 301 CCTGTGGAGGAGGAGTCTGCAACCTATTACTGTTCAGACAGACTAGGGAGATCCGTAC 360  
 Db 384 acgttcgaggggggacccaagctggaataaaa 416  
 Qy 361 ACCTTCGGAGGGGGGACCAACCTGGAATAAAA 393

RESULT 6

LOCUS MUSIGKPSV 526 bp mRNA ROD 29-OCT-1994  
DEFINITION Mus musculus processed pseudo-IgK chain mRNA, VC-region, from hybridoma A23A41.  
ACCESSION L02345  
KEYWORDS C-region; V-region; immunoglobulin kappa-chain; immunoglobulin light chain; pseudogene.  
SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) cDNA to mRNA.  
ORGANISM Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS Kaluzs,B., Betzl,G., Shao,H., Diamantstein,T. and Weidle,U.H.  
TITLE A general method for chimerization of monoclonal antibodies by inverse polymerase chain reaction which conserves authentic N-terminal sequences  
JOURNAL Gene 122 (2), 321-328 (1992)  
MEDLINE 93138402  
COMMENT NCBI gi: 197370  
FEATURES  
source Location/Qualifiers  
1..526  
/organism="Mus musculus"  
/strain="BALB/c"  
/sub\_species="domesticus"  
/cell\_line="hybridoma A23A41"  
/sequenced\_mol="cDNA to mRNA"  
96..>526  
/gene="pseudo-IgK"  
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/codon\_start=1  
98..157  
/gene="pseudo-IgK"  
/codon\_start=1  
158..489  
/gene="pseudo-IgK"  
mat\_peptide 158..>526  
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490..>526  
/gene="pseudo-IgK"  
/note="This CDS feature is included to show the translation of the corresponding C\_region. Presently translation qualifiers on C region features are illegal."  
/translation="ADAAPTGVIFQAX"  
490..>526  
C\_region 121 a 157 c 122 g 126 t  
BASE COUNT 121 a 157 c 122 g 126 t  
ORIGIN  
Query Match 87.8%; Score 345; DB 56; Length 526;  
Best Local Similarity 96.4%; Pred. No. 0.00e+00;  
Matches 379; Conservative 0; Mismatches 10; Indels 4; Gaps 2;  
Db 98 atggagacacacactggttactggtgactgctgctggtggttcactggttccactggt 157  
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QY 1 ATGGAGTCACACACACTCTGCTGATGGGTACTGCTGCTCTGGGTCCAGGGTTCACCTGGT 60  
Db 158 gacattgtgctgacacagtctcctgcttcttagctgtatctctggtgggcagagggccacc 217  
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QY 61 GACATTGTGCTGACACAGTCTCCTCTTAGGTGTATCTCTGGGCGACAGGGCCACC 120  
Db 218 atctcatcagggccagcaaaagtctcagtcacatctggctatgattatgactcagtggaac 277  
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QY 121 ATCTCATCGCGCCGACGMAAGTGTCACTACATCTGGCTATAGTTATATGCATCGGTAC 180

Db 278 caacagaacaggacagccaccagactcctcatctatcttctgtatccaacctagaatct 337  
QY 181 CAACAGAAACCAGGACAGACACCCAAACTCCTCATCTATCTTGCATCCACCTAGAACTCT 240  
Db 338 ggggtccctgccagttcagtgagtcgggtctgggacagacttcacctccaacatcat 397  
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QY 241 GGGTCCCTGCCAGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300  
Db 398 cctgtggaggaggagtgctgcaacctattactgtcagcaccattaggagc-t---tac 453  
||||| |  
QY 301 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCACAGTAGGGAGATCCGTAC 360  
Db 454 acgttcggaggggggaccgaagtctggaataaaa 486  
||||| |  
QY 361 ACCTTCGGAGGGGGACCAAGCTGGAATAAAA 393  
RESULT 7  
LOCUS MUSIGKADK 336 bp mRNA ROD 24-JUL-1990  
DEFINITION Mouse Ig rearranged kappa-chain mRNA V-J region, partial cds.  
ACCESSION M36755  
KEYWORDS J-region; V-region; immunoglobulin light chain; processed gene.  
SOURCE Mouse (strain Balb/c), cDNA to mRNA, anti-influenza hemagglutinin hybridoma H37-68 Vk.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 336)  
AUTHORS Clarke,S.H., Rickert,R., Wloch,M.K., Staudt,L.M., Gerhard,W. and Weigert,M.  
TITLE The BALB/c secondary response to the Sb site of influenza virus hemagglutinin  
JOURNAL J. Immunol. 145, 2286-2296 (1990)  
MEDLINE 90375929  
COMMENT Draft entry and computer-readable sequence for [J. Immunol. (1990) in press] kindly submitted by S.H.Clarke, 18-JUL-1990.  
FEATURES  
source Location/Qualifiers  
1..336  
/organism="Mus musculus"  
<1..>336  
/note="Ig H-chain V-J-region; NCBI gi: 196610"  
/codon\_start=1  
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GQSPKLLIYLASNLESGVPXRFSGSGGTFTLTIHPVEEDDAATYYCQHSRELPYTF  
GGGKLEIKR"  
BASE COUNT 85 a 89 c 82 g 77 t 3 others  
ORIGIN Chromosome 6.  
Query Match 79.4%; Score 312; DB 56; Length 336;  
Best Local Similarity 96.4%; Pred. No. 0.00e+00;  
Matches 321; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
Db 1 gacattgtgtgacacagtctcctgcttcttactgtattcttctggggcagagggccacc 60  
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QY 61 GACATTGTGCTGACACAGTCTCTGCTTCTCTTAGGTGTATCTCTGGGCGACAGGGCCACC 120  
Db 61 atctcatcagggccagcaaaagtctcgtctatctgactatagttatgactcagtggtac 120  
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QY 121 ATCTCATCGCGCCGACGMAAGTGTCACTACATCTGGCTATAGTTATATGCATCGGTAC 180  
Db 121 caacagaacaggacagtcacccaactcctcatctatcttctgcatccaacctagaatct 180

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Qy 181 CAACAGAAACGAGGACAGACACCAAACTCTCATCTATCTTCATTCACACCTAGAACTCT 240  
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Db 181 ggggtccctnccaggttcagtnccagtggtgtcggagacagattccaccccaacatccat 240  
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Qy 241 GGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300  
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Db 241 cctgtggagaggaggtgctgcaacctattactgtcagcacagtagtagggaggttcctgac 300  
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Qy 301 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTGACACAGTAGGAGAAATCCGTAC 360  
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Db 301 acgttcggagggggaccagagctggaataaaa 333  
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Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAATAAAA 393  
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RESULT 8  
LOCUS MMT3VL 333 bp DNA ROD 05-DEC-1993  
DEFINITION M. musculus anti-T3 980Q variable light chain.  
ACCESSION X67467 S40893  
KEYWORDS light chain; monoclonal antibody; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 333)  
AUTHORS Thammana, P., Gaito, A.L. and Largen, M.T.  
TITLE Sequences of variable regions of a monoclonal antibody specific to the thyroid hormone, triiodo-L-thyronine  
JOURNAL Mol. Immunol. 29 (7-8), 1025-1028 (1992)  
MEDLINE 92342145

COMMENT NCBI gi: 395286  
FEATURES  
source  
1..333  
Location/Qualifiers  
/organism="Mus musculus"  
/sex="female"  
/strain="CBA/J"  
/cell\_line="hybridoma 980Q"  
/sub\_clone="980Q 321.22.32.12"  
<1..>333  
/note="light chain"  
/product="anti-T3 antibody 980Q"  
BASE COUNT 83 a 91 c 83 g 76 t  
ORIGIN

Query Match 78.1%; Score 307; DB 54; Length 333;  
Best Local Similarity 96.1%; Pred. No. 1.25e-297;  
Matches 320; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 1 gacattgtgtgacagctctctgtcttcttagtgtatctctggggcagagggccacc 60  
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Qy 61 GACATTGTGTGTGACAGCTCTCTGTTCTTAGGTGTATCTCTGGGGCAGAGGGCCACC 120  
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Db 61 atctcatgagggccagcaaaagtctcagtagcatctcggtctatgttatgcactggtac 120  
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Qy 121 ATCTATCATGAGGCCAGCAAAAGTGTGAGTACATCTGGCTATGCTATATATCATCGTGTAC 180  
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Db 121 caacagaacacgagcagcaacccaaacctctcatctatctttgtcacaactagatct 180  
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Qy 181 CAACAGAACGAGGACAGACACCAAACTCTCATCTTTCATTCACACCTAGAACTCT 240  
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Db 181 ggggtccctgcaggttcagtgagctgggtctgggacagacctccacctcaacatccat 240  
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Qy 241 GGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300  
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Db 241 cctgtggagaggaggtgctgcaacctattactgtcagcacagtagggaggttctctccg 300  
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Qy 301 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTGACACAGTAGGAGAAATCCGTAC 360  
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Db 301 acgttcgggtggagccaccaagctggaatacaa 333  
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Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAATAAAA 393  
|||||

RESULT 9  
LOCUS MMIGVK20P 690 bp DNA ROD 17-FEB-1995  
DEFINITION M.musculus Ig Vkappa-pseudo-HNK20 gene.  
ACCESSION X82689  
KEYWORDS immunoglobulin; kappa light chain; pseudogene; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 690)  
AUTHORS Berdoz, J. and Kraehenbuhl, J.P.  
TITLE Specific amplification by the polymerase chain reaction of rearranged genomic variable regions of immunoglobulin genes from mouse hybridoma cells

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 690)  
AUTHORS Berdoz, J.A.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-1994) to the EMBL/GenBank/DBJ databases. J.A. Berdoz, Swiss Institute for Experimental Cancer Research, 155 ch. des Boveresses, 1066 Epalinges, SWITZERLAND

COMMENT NCBI gi: 673445  
FEATURES  
Location/Qualifiers  
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1..65  
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66..303  
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304..647  
/number=2  
315..647  
/product="variable region of the Ig kappa light chain"  
648..690  
/number=2  
BASE COUNT 171 a 169 c 155 g 195 t  
ORIGIN

source  
1..690  
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/cell\_line="HNK20"  
1..65  
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648..690  
/number=2  
BASE COUNT 171 a 169 c 155 g 195 t  
ORIGIN



sig_peptide	61..109 /note="Ig kappa V-region 1.5kb-V-kappa signal peptide" /codon_start=1 61..109
exon	/note="Ig kappa V-region 1.5kb-V-kappa, exon 1; putative" join(61..109,351..361)
sig_peptide	/note="Ig kappa V-region 1.5kb-V-kappa signal peptide" /codon_start=1 110..350
intron	/note="VK1.5 intron A" 351..658
exon	/note="Ig kappa V-region 1.5kb-V-kappa, exon 2; putative" 351..361
sig_peptide	/note="Ig kappa V-region 1.5kb-V-kappa signal peptide" /codon_start=1 351..>659
exon	/note="Ig kappa V-region 1.5kb-V-kappa" /number=2 351..361
exon	/note="Ig kappa V-region 1.5kb-V-kappa signal peptide, exon 2; putative" 362..659
mat_peptide	/partial /note="Ig kappa V-region 1.5kb-V-kappa mature peptide" /codon_start=1 660..>706
iDNA	/note="V-J Intervening DNA (5' end +/- 1 bp)"

BASE COUNT	175 a	178 c	156 g	197 t	
ORIGIN	1 bp upstream of EcoRI site on chromosome 6.				
	Query Match 77.6%; Score 305; DB 56; Length 706;				
	Best Local Similarity 98.7%; Pred. No. 2.07e-295;				
	Matches 309; Conservative 0; Mismatches 4; Indels 0; Gaps 0;				
Db	345	ttccaggttccactggtgacattgctgacacagtcctcctgcttccttagctgtatctc	404		
Qy	44	ttccaggttccactggtgacattgctgacacagtcctcctgcttccttagctgtatctc	103		
Db	405	tggggcagagggccacatctcatgaggccagcaaaagtgcagtaacatctggctata	464		
Qy	104	tggggcagagggccacatctcatgaggccagcaaaagtgcagtaacatctggctata	163		
Db	465	gttatatgactggtaccacagaaaaccgagcagcaccacccaaactcctcatctctg	524		
Qy	164	gttatatgactggtaccacagaaaaccgagcagcaccacccaaactcctcatctctg	223		
Db	525	catccaaactagaatctggggtccctgccaggttcagtgccagtggtctggacagact	584		
Qy	224	catccaaactagaatctggggtccctgccaggttcagtgccagtggtctgggacagact	283		
Db	585	tcacctcaactccatcctctggagaggaggatgctgcaacctattactgtcagcaca	644		
Qy	284	tcacctcaactccatcctctggagaggaggatgctgcaacctattactgtcagcaca	343		
Db	645	gtaggagacttcc	657		
Qy	344	gtaggagaaatcc	356		
RESULT	11				
LOCUS	WMIG21F5	666 bp	DNA	ROD	04-AUG-1992

04-AUG-1992

DEFINITION Mouse Ig light chain V(kappa)2IE-J(kappa)5 rearranged DNA, non-functional.

ACCESSION X13938 Y00804

KEYWORDS Ig kappa light chain; Ig light chain; immunoglobulin; pseudogene; rearranged DNA; variable region.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 666)

AUTHORS Mueller, B.

TITLE Direct Submission

JOURNAL Submitted (09-JAN-1989) to the EMBL/GenBank/DBJ databases. Mueller B., Institut fuer Genetik, Weyertal 121, 5000 Koeln 41, FRG

REFERENCE 2 (bases 466 to 666)

AUTHORS Muller, B. and Reth, M.

JOURNAL Ordered activation of the Ig lambda locus in Abelson B cell lines J. Exp. Med. 168 (6), 2131-2137 (1988)

MEDLINE 89067821

COMMENT the correctly rearranged V(kappa)2IE segment is not functional because it carries a 1-bp deletion in the leader sequence Data kindly reviewed (28-NOV-1990) by Mueller B.

NCBI gi: 51649 Location/Qualifiers

source 1..666

/organism="Mus musculus"

/strain="NIH/Swiss"

/cell\_line="B1p8-7b Abelson 300-19"

/chromosome="6."

misc\_feature 60..107

/note="V(kappa)2IE leader"

misc\_feature 341..646

/note="V(kappa)2IE exon"

misc\_feature 647..666

/note="J(kappa)5 region"

BASE COUNT 160 a 167 c 151 g 188 t

ORIGIN

Query Match 77.1%; Score 303; DB 53; Length 666;

Best Local Similarity 98.4%; Pred. No. 3.42e-293;

Matches 308; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 335 ttccaggttcactggagacattgtgtgcacagtcctctgttcccttagctgtatctc 394

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Qy 44 TTCAGGTTCCACTGGTGACATTGCTGTGACACAGTCCTCTTCTTAGGTATCTC 103

Db 395 tggggcagagggccaccattctcatgcaggccagcaaaagtgtcagcacatctggctata 454

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Qy 104 TGGGCGACAGGGCCACCATTCTCATGACGGCGCAGCAAAAGTGTCACTATCTGGCTATA 163

Db 455 gttatatgactgttaccacagaaccaggacagccaccaactcctcatctatctttg 514

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Qy 164 GTTATATGACTCGTACCAACAGAACCCAGGACAGACACCCCAACTCTCATCTATCTTG 223

Db 515 catccaactagaaatctgggttcctgccaggttcagtgccagtggttcgtggacagact 574

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Qy 224 CATCAACACTAGAAATCGGGGTCCCTCCAGGTTCACTGGCAGTGGGCTGGGACAGACT 283

Db 575 tcacctcaacatccatcctgtggagaggaggatgtgcaacctattactgtcagcaca 634

Qy 284 TCACCTCAACATCATCTCTGTGGAGGAGGAGATGCTGCAACCTATTACTGTGACACA 343

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Db 635 gtaggagctctcc 647

|||||

Qy 344 GTAGGAGAAATCC 356

|||||

RESULT 12

LOCUS MDIGKVBI 333 bp RNA ROD 05-NOV-1994

DEFINITION M.domesticus Igk variable region.

ACCESSION 222098

KEYWORDS anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.

SOURCE western European house mouse.

ORGANISM Mus musculus domesticus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 333)

AUTHORS Tillman, D.M., Jou, N.T., Hill, R.J. and Marion, T.N.

TITLE Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice

JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)

MEDLINE 92381444

REFERENCE 2 (bases 1 to 333)

AUTHORS Marion, T.N.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-1993) to the EMBL/GenBank/DBJ databases. Tony N. Marion, Microbiology and Immunology, University of, Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA

COMMENT NCBI gi: 297663

FEATURES

source 1..333

/organism="Mus domesticus"

/strain="(NZB x NZW)F1"

/dev\_stage="somatic variant"

/tissue\_type="spleen"

/cell\_type="hybridoma"

/cell\_line="17s.16"

/isolate="mouse #17"

/chromosome="6"

/sex="Female"

<1..>333

/gene="Igk"

/note="17s.16 is clonally related to the IgG hybridomas 17s.94 and 17s.124 in clone 17s-c4. NCBI gi: 297664"

/codon\_start=1

/function="kappa light chain variable region for anti-DNA antibody; Vk21 family"

/product="immunoglobulin variable region"

/translation="DIVLTQSPASLAVSIGQRATISCRASQSVSTAYSIIHWYQKRP

QQTPELLIKYASNLDSGVPARFSCSGTDFITINHPVEEDTATYYCQHSWEIPFTF

GGGTGLEIK"

BASE COUNT 88 a 87 c 82 g 75 t 1 others

ORIGIN

Query Match 76.6%; Score 301; DB 53; Length 333;

Best Local Similarity 94.9%; Pred. No. 5.65e-291;

Matches 316; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Db 1 gacattgtcacacagtctctgttcccttagctgtatctctgtgggacagggccacc 60

|||||

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17

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QY 61 GACATTGTGTCACACAGCTCTCTGCTTCTTAGGTGTAATCTCTGGGCGACAGGGCCACC 120
Db 61 atctcatgcaggccagcaaaagtcagvacatctgctactatgtattatattcaactggtac 120
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QY 121 ATCTCATGCGAGGCCAGCAAAAGTCTGATACATCTGCTATAGTATATATGCACTGGTAC 180
Db 121 caacgaaccaggacagacacccaaactcctcatcaagtatgcattccaacctagattct 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 181 CAACAGAACACGACAGACACACCCAAACTCTCTATCTTTCATTCACACTAGAAATCT 240
Db 181 ggggtccctaccagttcagtgccatgggtctgggacagacttcaacctcaacatccat 240
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QY 241 GGGGTCCCTGCCAGGTTCACTGGCAGTGGGCTTGGCAGACAGTTCACCCCTCAACATCCAT 300
Db 241 cctgtggagagagatgatactgcaacataattactgtcagacagagttgggagattccggtt 300
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QY 301 CTGTGAGGAGGAGGATGCTGCAACCTATTACTGTACAGACAGTAGGAGAAATCCGTAC 360
Db 301 acgttcggaggggggaccaaactggaaataaaa 333
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QY 361 ACCTTCGAGGGGGGACCAAGCTGGAATAAAA 393
```

```
RESULT 13
LOCUS MW1013 333 bp RNA ROD 05-AUG-1995
DEFINITION Mouse mRNA for kappa-immunoglobulin light chain V-J region (cell
line 103-7E).
ACCESSION X51851
KEYWORDS Ig kappa light chain; Ig light chain; immunoglobulin;
joining region; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Osteichthyes; Sarcoterygii; Mammalia; Eutheria;
Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 333)
AUTHORS Reininger,L.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-1990) to the EMBL/GenBank/DBJ databases.
Reininger L., Dept of Pathology , Centre Medical Universitaire, 1
rue michel servet, CH-1211 Geneve 4, Switzerland
REFERENCE 2 (bases 1 to 333)
AUTHORS Reininger,L., Shibata,T., Ozaki,S., Shirai,T., Jatoni,J.C. and
Izui,S.
TITLE Variable region sequences of pathogenic anti-mouse red blood cell
autoantibodies from autoimmune NZB mice
JOURNAL Eur. J. Immunol. 20 (4), 771-777 (1990)
MEDLINE 90269328
COMMENT NCBI gi: 55392
FEATURES Location/Qualifiers
source 1..333
/organism="Mus musculus"
/strain="New Zealand black"
/cell_type="hybridoma B"
/cell_line="103-7E"
<1..>333
/note="kappa-Ig light chain (111 AA)"
V_region <1..>333
/note="pid:e20960; NCBI gi: 930228"
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GGPKLIKVASNLESVPARTSGSGCTDTLNIHPVEEDTATYYQHSWEIPTF
GGTKLEIK"
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Jul 8 08:22

US-08-137-117B-24.rge

18

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BASE COUNT 85 a 86 c 86 g 75 t 1 others
ORIGIN
Query Match 76.3%; Score 300; DB 55; Length 333;
Best Local Similarity 94.9%; Pred. No. 7.26e-290;
Matches 316; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Db 1 gacattgttgacacagtcctcgttcttcttagctgtatcgtctgggnagagggccaacc 60
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QY 61 GACATTGCTGCACACAGTCTCTGCTTCTTAGGTGTAATCTCTGGGCGACAGGGCCACC 120
Db 61 ctctcatgcaggccagccaaagtgtcagttctatctggtctatgtatgtatgtacactggtac 120
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QY 121 ATCTCATGCGAGGGCGACAAAAGTGTGATACATCTGGCTATAGTATATATGCACTGGTAC 180
Db 121 caacgaaccaggacagtcacccaactcctcatcaagtatgcattccaacctagaatct 180
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QY 181 CAACAGAACACGACAGACACCCAAACTCTCTATCTTTCATTCACACTAGAAATCT 240
Db 181 ggggtccctgccagttcagtgccagtggtctgggacagacttcaacctcaacatccat 240
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QY 241 GGGGTCCCTGCCAGGTTCACTGGCAGTGGGCTTGGGACAGACTTCACCCCTCAACATCCAT 300
Db 241 cctgtggagagagatgatactgcaacataattactgtcagacagttgggagattccggtc 300
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QY 301 CTGTGAGGAGGAGGATGCTGCAACCTATTACTGTACAGACAGTAGGAGAAATCCGTAC 360
Db 301 acgttcggaggggggaccaaactggaaataaaa 333
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 361 ACCTTCGAGGGGGGACCAAGCTGGAATAAAA 393
```

```
RESULT 14
LOCUS MMU01973 394 bp mRNA ROD 24-SEP-1993
DEFINITION Mus musculus Balb/c anti-CD18 Ig light chain variable region mRNA,
partial cds.
ACCESSION U01973
KEYWORDS mouse.
SOURCE Mus musculus
ORGANISM Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Rodentia; Myomorpha; Muridae; Mus.
REFERENCE 1 (bases 1 to 394)
AUTHORS Hsiao,K., Bajorath,J. and Harris,L.J.
TITLE Humanization of 60.3, an anti-CD18 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 394)
AUTHORS Harris,L.J.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1993) Linda J. Harris, Molecular Immunology,
Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First
Avenue, Seattle, WA 98121 USA
COMMENT NCBI gi: 403071
FEATURES Location/Qualifiers
source 1..394
/strain="Balb/c"
/organism="Mus musculus"
/cell_line="60.3 hybridoma"
/cell_type="hybridoma (B-cell)"
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/dev_stage="adult"
1..60
/note="nucleotides 1-29 derived from PCR primer and may
not reflect mRNA sequence"
sig_peptide
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exon      1..49
/product="partial signal peptide"
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CDS       1..394
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Jk1; NCBI gi: 403072"
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EADDAVATYCCQSNEDPTFPGGTRKLEIK"
50..394
exon      /number=2
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chain"
misc_feature 61..135
/standard_name="FR1"
mat_peptide 61..393
/product="Ig variable region, light chain"
misc_feature 136..168
/standard_name="CDR1"
misc_feature 169..219
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misc_feature 220..228
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BASE COUNT 99 a 100 c 98 g 97 t
ORIGIN

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[illegible]

Qy	361	ACGTTCCGAGGGGGACCAAGCTGGAATAAAAA	393
RESULT	15		
LOCUS	MUSICKAAS	339 bp	mRNA
DEFINITION	Mouse immunoglobulin aberrantly rearranged kappa-chain mRNA		30-JUN-1987
ACCESSION	V138J2-region from hybridoma	CEA 66-E3.	
KEYWORDS	MI4435		
SOURCE	C-region; J-region; V-region; immunoglobulin-kappa; processed gene; pseudogene.		
ORGANISM	Mouse hybridoma CEA 66-E3, cDNA to mRNA.		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.		
TITLE	1 (bases 1 to 339)		
JOURNAL	Immunoglobulin transcripts and molecular history of a hybridoma that produces antibody to carcinoembryonic antigen		
MEDLINE	Gene 40, 157-161 (1985)		
COMMENT	86137415		
	A 4 nt deletion at the V-J recombination site causes misalignment of the V and J segments resulting in a nonfunctional kappa-chain.		
FEATURES	NCBI gi: 196462		
source	Location/Qualifiers		
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	<1..6		
	/note="pseudo-Igk leader pept"		
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	/codon start=1		
CDS	<1..>339		
	/note="pseudo-Igk precursor"		
	/pseudo		
	/codon start=1		
mat_peptide	7...>339		
	/note="pseudo-Igk"		
	/codon start=1		
BASE COUNT	87 a 90 c 86 g 76 t		
ORIGIN	Chromosome 6.		
Query Match	75.3%; Score 296; DB 56; Length 339;		
Best Local Similarity	95.9%; Pred. No. 1.97e-285;		
Matches	325; Conservative 0; Mismatches 11; Indels 3; Gaps 2;		
Db	1	actggtgacattgtgtgacacagtcctctgcttcttagctgtatctctgggcagagg	60
Qy	55	ACTGGTGCAATTGCTGCACAGCTCCTGCTTCTTAGGGTATCTCTGGGGCAGAGG	114
Db	61	gccaccatctcatcacaggccagcaagtgtcagatccttggtatagttatgtcac	120
Qy	115	GGCACCATCTCATCGAGGGCGACAAAGTGTCAGTGACATCTGGGCTATGTTATG	174
Db	121	Tggaaaccaagaacaacagcaccagactcctcatctatcttgatccaacct	180
Qy	175	TGGTATCCAAAGAAACACAGACAGACACCAAACTCCTCATCTATCTTGCATCCA	234
Db	181	gaatctggggctccctgccagggttcagtgccagtggtctgggacagacttcacct	240
Qy	235	GAATCTGGGGTCCCTGCCAGGTTCACTGGCAGCTGGGCTCTGGGACAGACTTCA	294
Db	241	atccatctgtggaggaggaggtggtgcaacctattactgtcagcacattagg-gag-	298

21

Qy 355 CCGTACACGTTCCGAGGGGGACCAAGCTGGAAAATAAAA 393

Search completed: Mon Jul 8 08:33:17 1996  
Job time : 351 secs.

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

Statistics: Mean 10.000; Variance 1.898; scale 5.268

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES


Result No.	Score	Match	Query Length	DB	ID	Description	Pred. No.
1	123	31.3	488	11	H25625	y148g05.r1 Homo sapie	4.04e-198
2	105	26.7	467	12	H27034	y145d05.r1 Homo sapie	1.74e-160
3	104	26.5	364	127	HST72579	EST100049 Homo sapien	2.06e-158
4	104	26.5	364	69	T27519	EST100049 Homo sapien	2.06e-158
5	93	23.7	470	114	HS115213	yu40h01.r1 Homo sapie	9.43e-136
6	93	23.7	470	97	H62115	yu40h01.r1 Homo sapie	9.43e-136
7	92	23.4	359	127	HST72587	EST100475 Homo sapien	1.05e-133
8	92	23.4	359	69	T27587	EST100475 Homo sapien	1.05e-133
9	88	22.4	357	70	T29104	EST69270 Homo sapiens	1.50e-125
10	88	22.4	357	114	HS10412	EST69270 Homo sapiens	1.50e-125
11	86	21.9	445	47	R48141	yf66c09.r1 Homo sapie	1.72e-121
12	85	21.6	381	114	HS11411	EST69430 Homo sapiens	1.83e-115
13	85	21.6	381	70	T29114	EST69430 Homo sapiens	1.83e-115
14	85	21.6	430	115	HS156227	yr86f06.r1 Homo sapie	1.83e-119
15	85	21.6	430	98	H69156	yr86f06.r1 Homo sapie	1.83e-119
16	84	21.4	503	41	R28232	yh57e08.r1 Homo sapie	1.93e-117
17	83	21.1	383	70	T29916	EST99871 Homo sapiens	2.02e-115
18	83	21.1	383	125	HS91615	EST99871 Homo sapiens	2.02e-115
19	83	21.1	463	53	R69532	yj82d09.r1 Homo sapie	2.02e-115
20	82	20.9	383	69	T27870	EST19007 Homo sapiens	2.09e-113
21	82	20.9	383	127	HST27870	EST19007 Homo sapiens	2.09e-113
22	77	19.6	210	53	R69482	yj83c03.r1 Homo sapie	2.24e-103
23	77	19.6	393	69	T27593	EST100653 Homo sapien	2.24e-103
24	77	19.6	393	127	HST27593	EST100653 Homo sapien	2.24e-103
25	76	19.3	332	118	HS34210	EST77181 Homo sapiens	2.22e-101
26	76	19.3	332	70	T29342	EST77181 Homo sapiens	2.22e-101
27	76	19.3	390	17	H45841	yp22b04.r1 Homo sapie	2.22e-101
28	76	19.3	390	124	HS841242	yp22b04.r1 Homo sapie	2.22e-101
29	76	19.3	438	51	R64693	yi22f09.r1 Homo sapie	2.22e-101
30	75	19.1	434	87	T39178	yi22f09.r1 Homo sapie	2.22e-101
31	73	18.6	203	15	H93743	yo53d07.r1 Homo sapie	2.03e-95
32	73	18.6	279	70	T29656	EST89211 Homo sapiens	2.03e-95
33	73	18.6	279	122	HS65610	EST89211 Homo sapiens	2.03e-95
34	73	18.6	516	52	R67559	yi42h11.r1 Homo sapie	2.03e-95
35	69	17.6	359	12	H27642	yf61g07.r1 Homo sapie	1.59e-87
36	68	17.3	408	58	R60635	yp12g07.r1 Homo sapie	1.44e-85
37	68	17.3	451	86	T90236	ye15d10.r1 Homo sapie	1.44e-85
38	66	16.8	257	48	RS1193	yf17a07.r1 Homo sapie	1.17e-81
39	66	16.8	397	47	R49771	yf55c03.r1 Homo sapie	1.17e-81
40	65	16.5	261	46	R46878	yj34h03.r1 Homo sapie	1.03e-79
41	64	16.3	570	53	T70290	yj81d08.r1 Homo sapie	8.99e-78
42	64	16.0	360	56	R79907	yi85f01.r1 Homo sapie	7.74e-76
43	63	16.0	395	70	T29112	EST69384 Homo sapiens	7.74e-76
44	63	16.0	395	114	HS11211	EST69384 Homo sapiens	7.74e-76
45	62	15.8	141	15	R39551	yf67h12.r1 Homo sapie	6.59e-74

## ALIGNMENTS

RESULT	1				
LOCUS		H25625	488 bp	mRNA	EST
					10-JUL-1995

\*\*\*\*\*

(M)

1.      

[illegible]

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPerch nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:34:42 1996; MasPar time 182.60 Seconds  
773.735 Million cell updates/sec

Tabular output not generated.

Title: >US-08-137-117B-24

**Description.**  
**Perfect Score:**

Sequence: 1 ATGGAGTCAGACACACTCCT.....GGACCAAGCTGGAAATAAAA 393  
Comp: TACCTCACTCTGTGTGAGGA.....CCTGGTTCGACCTTTATTTT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
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93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98  
99:EST99 100:EST100

Database:

95: gneST11 96: gneST2 97: gneST3 98: gneST4 99: gneST5  
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110: gneST5 111: gneST6 112: gneST7 113: gneST5 114: gneST6  
115: gneST7 116: gneST8 117: gneST9 118: gneST10 119: gneST11  
120: gneST12 121: gneST13 122: gneST14 123: gneST15  
124: gneST16 125: gneST17 126: gneST18 127: gneST19









TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pTT3 vector (Pharmacia). Library  
constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 470)

## AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and  
Wilson,R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
High quality sequence stops: 354  
Source: IMAGE Consortium, LIND  
This clone is available royalty-free through LIND; contact the  
IMAGE Consortium (info@image.lind.gov) for further information.

NCBI gi: 1014947

## FEATURES

Location/Qualifiers

source

1..470

/organism="Homo sapiens"

/clone="236305"

mRNA

<1..>470

BASE COUNT

112 a 108 c 119 g 120 t 11 others

ORIGIN

Query Match

Best Local Similarity 23.7%; Score 93; DB 97; Length 470;

Matches 160; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Db 19 tatttngactggtaacctgcagaagccaggcgagtcctccacagctcgtatatacgtt 78

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Qy 166 TATATGCACCTGGTACACACAGAACACGACAGACACACCACTCTCATCTATCTGCA 225

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Db 79 tctatcggccctctgcagtcaccagacaggttcagtgccagtggtggtcaggaactgattc 138

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 226 TCACACCTAGATCTGGGGTCCCTGCCAGTTGAGTGGCAGTGGGCTGGGACAGACTTC 285

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Db 139 acactgaaatcagcaggggtggaggtcagatgttgagttattactgcagcaact 198

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Qy 286 ACCCTCAACATCCATCCCTGTGGAGAGGAGGATGCTGCAACCTATTACTGACGACAGT 345

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Db 199 atagagtttcttggaacttttggcaggaggggacccaagctggagatcaaa 246

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Qy 346 AGCGAATCCGTACACCTCGGAGGGGGGACCAACGACTCGAATAAATA 393

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7

ID HST27587

AC T27587; standard; RNA; EST; 359 BP.

DT 12-JAN-1995 (Rel. 42, Created)  
DT 07-SEP-1995 (Rel. 45, Last updated, Version 2)  
DE EST100475 Homo sapiens cDNA 5' end similar to immunoglobulin kappa  
light chain V region (GB:X63397) (HT:3865).  
KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

RN [1]

RP 1-359

RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

RA Bult C.J., Lee N., Kirkness E.F., Weinstein K.G., Gocayne J.D.,

RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,

RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,

RA FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geohagen N.S.M.,

RA Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,

RA Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,

RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,

RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,

RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,

RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,

RA Flescher C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,

RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,

RA Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,

RA Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,

RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;

RT \*Initial Assessment of Human Gene Diversity and Expression

Patterns Based Upon 52 Million Basepairs of cDNA Sequence";

RL Unpublished.

CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper

CC Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:

CC tdbinfo@db.tigr.org For clone availability, additional sequence

and expression information related to this EST, please contact the

CC TIGR Database (tdbinfo@db.tigr.org). NCBI gi: 609685

Key Location/Qualifiers

FT source

1..359

/organism="Homo sapiens"

/note="human"

FT mRNA

<1..>359

SQ Sequence 359 BP; 75 A; 93 C; 95 G; 94 T; 2 other;

Query Match 23.4%; Score 92; DB 127; Length 359;

Best Local Similarity 68.1%; Pred. No. 1.05e-133;

Matches 207; Conservative 0; Mismatches 93; Indels 4; Gaps 4;

Db 25 ctctctggggctgaatgctctgggtctctggatccagtgagggtattgtctgactcag 84

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 19 CTGCTATGGGTACTGCTGCTGGGTTCCAGGTTCCACTGCTGCACATTGCTGCACAG 78

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 85 tctccactctccctgccgtaccctccctggagcgccgtttatctcctcaggtctagt 144

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 79 TCTCTCTCTTCTTAGGTGTATCTGTGGGCGAGGGCGCACCATCTCATCGAGGGCAGC 138

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 145 cagagactctcgtactgtaggacacaactatttggattggtacctgcagaagcagg 204

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Qy 139 AAAAGTCTCA-GTACA-T-CTGGCTATAGTTATATGCACCTGGTACCAAGAAACAGGA 195

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Db 205 cagtcctccacaactcctgatctatttgggttctaatacgggcctccggggtccctgacagg 264

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 196 CAGACACCCAAACTCCTCATCTATCTTGCATCCAACTAGAAATCTGGGGTCCCTGCCAGG 255

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Db 265 ttccagtggcagtggggtcaggccacagatitttaccactgaaaaaagcagagagtggaggtcga 324

Jul 8 08:27

US-08-137-117B-24.rst

11

QY 256 TTACGTGGCAGTGGG-TCTGGGACAGACTTCACCCCTCAACATCCATCTCTGTGGAGGAGGA 314  
|||||  
Db 325 gqat 328  
|||||  
QY 315 GGAT 318  
|||||

RESULT 8  
LOCUS T27587 359 bp mRNA EST 06-SEP-1995  
DEFINITION EST100475 Homo sapiens cDNA 5' end similar to immunoglobulin kappa  
light chain V region (GB:X63397) (HT:3865).

ACCESSION T27587  
KEYWORDS EST.  
SOURCE human primer=M13 Reverse library=Human Pancreas.  
ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 359)

ADAMS,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,  
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,  
Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,  
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S.,  
Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,  
Merrick,J.M., Moreno-Palancques,R.F., McDonald,L.A., Nguyen,D.T.,  
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,  
Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,  
Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,  
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,  
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,  
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,  
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,  
Yu,G.-L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A.,  
Haeeltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns  
JOURNAL Based Upon 52 Million Basepairs of cDNA Sequence  
COMMENT Unpublished (1995)

Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: tdbinfo@tdb.tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please contact the TIGR Database  
(tdbinfo@tdb.tigr.org).

FEATURES Location/Qualifiers

source  
1..359  
/organism="Homo sapiens"  
/note="human"

BASE COUNT 75 a 93 c 95 g 94 t 2 others  
ORIGIN

Query Match 23.4%; Score 92; DB 69; Length 359;  
Best Local Similarity 68.1%; Pred. No. 1.05e-133;  
Matches 207; Conservative 0; Mismatches 93; Indels 4; Gaps 4;

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12

Db 25 ctccctggggctgctaagtctctgggtctctggatccagtggggattattgtnctgactcag 84  
|||||  
QY 19 CTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGACATTTGGTGTGACACAG 78  
|||||  
Db 85 tctccactctccctgccqgnhacccctggagagcggcctttatctctgcaggtctagt 144  
|||||  
QY 79 TCTCCTGCTTCCTTTAGTGTATCTCTGGGGCAGAGGGCCACCATCTCATCGAGGGCCAGC 138  
|||||  
Db 145 cagagactctcgtactgactgacacacactatttgattggtacctgcagaagccagg 204  
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QY 139 AATAGTCTCA-GTACA-TCTGGCTATATTGATGCACTGGTGTACCAACAGAAACACGGA 195  
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Db 205 cagctctccaaactcctgactatttggttctaatcgggctcgggggtccctgcagcagg 264  
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QY 196 CAGACACCCCAACTCCTCATCTCTTTCATCCACCTAGAAATCTGGGGTCCCTGCCAGG 255  
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Db 265 ttccagtgcagtgaggatcaggcacagattttacactgaaaaataagcagagtgaggctga 324  
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QY 256 TTCACTGGCAGTGGG-TCTGGCAGACAGACTTCACCTCAACATCCATCCTCTGGAGGAGGA 314  
|||||  
Db 325 gqat 328  
|||||  
QY 315 GGAT 318  
|||||

RESULT 9  
LOCUS T29104 357 bp mRNA EST 06-SEP-1995  
DEFINITION EST69270 Homo sapiens cDNA 5' end similar to immunoglobulin kappa  
light chain V region (GB:X54248) (HT:3095).

ACCESSION T29104  
KEYWORDS EST.  
SOURCE human primer=M13 Reverse library=Human Lymphoid tissue.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 357)

ADAMS,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,  
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,  
Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,  
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S.,  
Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,  
Merrick,J.M., Moreno-Palancques,R.F., McDonald,L.A., Nguyen,D.T.,  
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,  
Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,  
Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,  
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,  
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,  
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,  
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,  
Yu,G.-L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A.,  
Haeeltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns  
JOURNAL Based Upon 52 Million Basepairs of cDNA Sequence  
COMMENT Unpublished (1995)

Other\_ESTs: EST69269  
Contact: Venter, JC

The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056

RA Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

SOURCE	FURNER - JAMES-193718
KEYWORDS	LAWRENCE-SERGEANT FURNEYA CARLUS
EST.	-1964-1967

RA Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

Db	172	ctggtaccagcagaaacttggccaggctccaggctctcatctatgatgcatacaacag	231
Qy	174	CTGGTACCAACAGAAAAACGACAGACACCCAACTCTCTATCTTGCATCCAGCT	233
Db	232	ggccgctggcatccacagacaggttcactggcagtgggctgggacagacttcactctcac	291
Qy	234	AGRAATCGGGTCCCTGGCAGGTCAGTGGCAGTGGCTGGGACGACTTCACCTCAA	293
Db	292	catcagcagacttggagcctgaagatatttggcagtgattatnctatcaaca	340

[illegible]

RESULT	13
LOCUS	T29114
DEFINITION	EST69430 Homo sapiens cDNA 5' end similar to immunoglobulin light chain V(HI), J(V) regions (GB:227170) (HT:3121).
	381 bp mRNA EST 06-SEP-1995

ACCESSION T29114  
KEYWORDS EST.

SOURCE human primer=M13 Reverse Library=Human Lymphoid tissue.  
ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Haplorhini; Hominidae; Homo

REFERENCE  
1 (bases 1 to 381)  
Eucneria; Alchornea; Filicites; Cactacanth; Homalium; Homalium; Homalium.

**AUTHORS**  
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,  
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.M.

FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geohagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,

Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancues, R.F., McDonald, L.A., Nguyen, D.T.

Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sautet, D.M., Shirlev, P., Small, K.V., Springs, T.A., Utterback, T.V.

Sauer, P.W., Sharkey, N., Smarr, R.V., Spriggs, L.M., Uccella, J.L., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.R., Collins, E.T., Dinko, D., Fong, B., Fox, A.

Coleman, I.A., Collins, E.-G., Dimke, D., Feng, F., Feller, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,

Grubert, J., Hudson, F., Kilm, A., Kozak, D. L., Kunsen, C., Jia, H., Li, Meissner, P. S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,

Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

**TITLE**  
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence

	JOURNAL	Unpublished (1995)	COMMENT
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Contact: Venter, JC  
The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878  
Tel. 3018600056

Tel: 3018699423  
 Fax: 3018699423  
 E-mail: [info@china-chemical.com](mailto:info@china-chemical.com)

Email: [cadm@roccab.tigr.org](mailto:cadm@roccab.tigr.org)  
For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org).

NCBI gi: 611212

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FEATURES
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Location/Qualifiers
  1..381

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/organism="Homo sapiens"  
/note="human"
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mRNA	BASE COUNT	others
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# ORIGIN

Query Match	21.6%;	Score 85;	DB 70;	Length 381;
Best Local Similarity	76.2%	Prod No	1 920 110.	

Best Local Similarity 76.3%; P-Filed. NO. 1.63E-113;  
Matches 129; Conservative 0; Mismatches 39; Indels 1; Gaps

**Db** 172 ctggtagcaggaacctggccaggctcccaggctcctcatctatgatgatccaacag 231

Qy 174 CTGGTACCAACAGAAACCCAGGACAGACACCCAACTCCTCATCTATCTTGCATCCAACT 233



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19

QY 196 CAGACACCAAACTCCTCATCTATCTTCGATCCAACTAGATCTGGGGTCCCTGCCAGG 255

Db 264 ttcaatggcagtnnggcaggagcagatttcacact 298  
||||| ||||| || ||||| ||||| ||

QY 256 TTCAGTGGCAGTGGGTCTGGGCACAGACTTCACCCCT 290

RESULT 15

LOCUS H69156 430 bp mRNA EST 19-OCT-1995  
DEFINITION yr86f06.r1 Homo sapiens cDNA clone 212195 5' similar to  
gb:XS5400\_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION  
(HUMAN); contains Alu repetitive element;;

ACCESSION H69156

KEYWORDS EST.

SOURCE human clone=212195 primer=M13R1 library=Soares fetal liver spleen  
INFLS vector=p7T3D (Pharmacia) with a modified polylinker  
host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver  
and spleen from a 20 week-post conception male fetus. 1st strand  
cDNA was primed with a Pac I - oligo(dT) primer [5'  
AACTGCAAGAAATAATAAGATCTTTTITTTTTTTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac  
I and cloned into the Pac I and Eco RI sites of the modified p7T3  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 430)  
Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfs, T., Soares, M., Tan, F.,  
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 267  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES NCBI gi: 1030482  
source Location/Qualifiers  
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/clone="212195"  
/note="human"  
mRNA <1..>430  
BASE COUNT 98 a 107 c 116 g 101 t 8 others  
ORIGIN

Query Match 21.6%; Score 85; DB 98; Length 430;  
Best Local Similarity 68.0%; Pred. No. 1.83e-119;  
Matches 187; Conservative 0; Mismatches 85; Indels 3; Gaps 3;

Jul 8 08:27

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20

Db 24 cttctggggctgctaatgctctgggtccctggatccagtggggataattgtgatgccacag 83  
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QY 19 CTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCAGTTGCTGCTGACACAG 78

Db 84 actccactctcctcaccctgtcaacccttggacagcggcctccatctctcgcaggtctagt 143  
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QY 79 TCTCTCTCTTCTTGGTGTATCTCTGGGGCAGAGGCCACCATCTCATGCAGGGCCAGC 138

Db 144 caaagcctctacacagtgatggaacacactacttggttgcttcagcagagggccaggc 203  
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QY 139 AAAAGTCTCAGT-ACA-TC-TGGCTATAGTTATATGCACTGGTACCAACAGAAACGAGGA 195

Db 204 cagcctccaagactcctaatattataagatttctaaccgggttctctggtgggtcccgacagaga 263  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 196 CAGACACCAAACTCCTCATCTATCTTCGATCCAACTAGATCTGGGGTCCCTGCCAGG 255

Db 264 ttcaatggcagtnnggcaggagcagatttcacact 298  
||||| ||||| ||| ||| ||||| ||| ||||| ||

QY 256 TTCAGTGGCAGTGGGTCTGGGCACAGACTTCACCCCT 290

Search completed: Mon Jul 8 08:38:06 1996  
Job time : 204 secs.

(TUL)

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Intelligenetics, Inc.

MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:28:23 1996; MasPar time 7.40 Seconds  
447.403 Million cell updates/sec

Tabular output not generated.

**Title:** >US-08-137-117B-25

Description: (1-131) from US08137117B, pep

Perfect Score: 942  
Sequence: 1 MESD<sup>T</sup>LLM<sup>V</sup>LLM<sup>V</sup>VPSTG.....COHSREN<sup>P</sup>YTFGGG<sup>T</sup>KLEIK 131

Scoring table: PAM 150  
Gap 11

Searched: 82306 seqs. 25270970 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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Database:
pir46
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1
13:unrev2
```

Statistics: Mean 41.173: Variance 148.737: scale 0.277

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	859	91.2	131	13	S55027		immunoglobulin light	2,53e-81
2	837	88.9	140	5	PN0446		Ig kappa chain precu	8,54e-79
3	819	86.9	131	2	KVMS66		Ig kappa chain precu	9,95e-77
4	806	85.6	132	2	KVMS32		Ig kappa chain precu	3,08e-75
5	805	85.5	131	5	PH1226		Ig kappa chain precu	4,01e-75
6	785	83.3	128	13	JI0073		aberrant kappa trans	7,84e-73
7	754	80.0	128	11	S52448		Ig kappa chain V reg	2,76e-69
8	741	78.7	111	2	KVMS84		Ig kappa chain V reg	8,41e-68
9	734	77.9	111	2	KVMS75		Ig kappa chain V reg	5,30e-67
10	725	77.0	111	2	KVMS40		Ig kappa chain V reg	5,63e-66
11	720	76.4	111	2	KVMS85		Ig kappa chain V reg	2,09e-65
12	713	75.7	112	12	S45715		antigen-Fab VL - pse	1,31e-64

## ALIGNMENTS

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RESTART      1
ENTRY        S55027 #type complete
TITLE        immunoglobulin light chain variable region precursor - mouse
             (fragment)
ORGANISM     #formal_name Mus musculus #common_name house mouse
DATE         23-Aug-1995 #sequence_revision 23-Aug-1995 #text_change
             23-Aug-1995
ACCESSIONS   S55027
REFERENCE    S55027
AUTHORS      Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.;
             Margolies, M.N.; Sheriff, S.
#journal     J. Mol. Biol. (1995) 248:344-360
#title       Structure and specificity of the anti-digoxin antibody 40-50
#accession   S55027
#status      preliminary
#residues    1-131 ##label JEF
##cross-references EMBL:L31404
SUMMARY      #length 131 #molecular-weight 14243 #checksum 6089

Query Match          91.2%; Score 859; DB 13; Length 131;
Best Local Similarity 91.6%; Pred. No. 2.53e-81;
Matches 120; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db      1 metdtilllwlllwpgstgdiivltcspaslavslqgraticraskvstsgyehihwy 60
QV      1 MESDTLLWLLWLLWPSTGTDIVLTQSPASISGLVSLQQRATISCRASKSVTSGYSYMHY 60

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Jul 8 08:18

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3

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Db 61 qqkpgppklllylasilesgvparfsgsgtdftlnihpveedaatyqcchereypl 120
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Db 121 tfgsgtelek 131
Qy 121 TFGGGTKLEIK 131

RESULT 2
ENTRY      PN0446      #type fragment
TITLE      Ig kappa chain precursor V-II region - human (fragment)
ORGANISM   #formal name Homo sapiens #common name man
DATE       30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
ACCESSIONS PN0446
REFERENCE   PN0444
#authors   Kaluza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidie,
            U.H.
#journal   Gene (1992) 122:321-328
#title     A general method for chimerization of monoclonal antibodies
            by inverse polymerase chain reaction which conserves
            authentic N-terminal sequences.
#accession PN0446
#molecule_type mRNA
#residues  1-140 ##label KAL
#cross-references GB:L02345
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS    immunoglobulin
FEATURE
1-20        #domain signal sequence #status predicted #label SIG
21-140      #product Ig light chain kappa-2 V region #status
            predicted #label MAT
SUMMARY     #length 140 #checksum 3597

Query Match      88.9%; Score 837; DB 5; Length 140;
Best Local Similarity 91.6%; Pred. No. 8.54e-79;
Matches 120; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

Db 1 metdtllllwllwvpgstgnivltqspaslgvslgqratiscrasksvstsgysymhwy 60
Qy 1 MESDTLLWLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYMHY 60

Db 61 qqkpgppklllylvnlesgvparfsgsgtdftlnihpveedaatyqcchire--l 118
Qy 61 QQKPGQTPKLLIYLASNLESVGPARGSGSGTDTLNIHPVEEDAATYYQCHSRENPY 120

Db 119 tfgggtkleik 129
Qy 121 TFGGGTKLEIK 131

RESULT 3
ENTRY      KWMSM6      #type complete
TITLE      Ig kappa chain precursor V regions (M63, AB22, PC9245,
            PC4050) - mouse
ORGANISM   #formal name Mus musculus #common name house mouse
DATE       02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
            31-Dec-1993
ACCESSIONS B90412; B90374; B93822; C93204; D93204; A01935
REFERENCE   A90412
#authors   Burstein, Y.; Schechter, I.
#journal   Biochemistry (1978) 17:2392-2400
#title     Primary structures of N-terminal extra peptide segments
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linked to the variable and constant regions of
immunoglobulin light chain precursors: implications on the
organization and controlled expression of immunoglobulin
genes.
#cross-references MUID:78235887
#contents   M63
#accession  B90412
#molecule_type protein
#residues   1-35 ##label BUR
REFERENCE   A90374
#authors   McKean, D.; Potter, M.; Hood, L.
#journal   Biochemistry (1973) 12:760-771
#title     Mouse immunoglobulin chains. Pattern of sequence variation
            among kappa chains with limited sequence differences.
#cross-references MUID:73140225
#contents   M63
#accession  B90374
#molecule_type protein
#residues   21-46, 'Q', 48-53, 'B', 55-57, 'Z', 59-86, 'F', 88-131 ##label
            MCK
#note      this sequence has since been revised in reference A93822
REFERENCE   A93822
#authors   McKean, D.J.; Bell, M.; Potter, M.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917
#title     Mechanisms of antibody diversity: multiple genes encode
            structurally related mouse kappa variable regions.
#cross-references MUID:79012520
#contents   M63; AB22
#accession  B93822
#molecule_type protein
#residues   1-53; 69-107 ##label MC2
#accession  C93822
#molecule_type protein
#residues   21-119, 'Y', 121-131 ##label MC3
REFERENCE   A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal   Nature (1978) 276:785-790
#title     Rearrangement of genetic information may produce
            immunoglobulin diversity.
#cross-references MUID:79073152
#contents   PC9245; PC4050
#accession  C93204
#molecule_type protein
#residues   21-119, 'Y', 121-131 ##label WEI
#accession  D93204
#molecule_type protein
#residues   21-119, 'L', 121-123, 'A', 125-129, 'L', 131 ##label WE2
COMMENT     The M63 precursor sequence is shown.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
1-20        #domain signal sequence #status experimental #label SIG
SUMMARY     #length 131 #molecular-weight 14291 #checksum 5945

Query Match      86.9%; Score 819; DB 2; Length 131;
Best Local Similarity 84.7%; Pred. No. 9.95e-77;
Matches 111; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Db 1 metdtllllwllwvpgstgnivltqspaslgvslgqratiscrasksvstsgysymhwy 60
Qy 1 MESDTLLWLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYMHY 60

Db 61 qqkpgppklllylaenlesgvparfsgsgtdftlnihpveedaatyqcqnnedpw 120
Qy 61 QQKPGQTPKLLIYLASNLESVGPARGSGSGTDTLNIHPVEEDAATYYCQHSRENPY 120
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Db 121 tfgggtkleik 131  
|||||  
Qy 121 TFGGGTKLEIK 131

RESULT 4  
ENTRY KVM52 #type complete  
TITLE Ig kappa chain precursor V regions (MOPC 321, TEPC 124) - mouse  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 31-May-1979 #sequence\_revision 31-May-1979 #text\_change 04-Nov-1994  
ACCESSIONS A90412; A90373; A90374; A01933  
REFERENCE A90412  
#authors Burstein, Y.; Schechter, I.  
#journal Biochemistry (1978) 17:2392-2400  
#title Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.

#cross-references MUID:78235887  
#contents MOPC 321  
#accession A90412  
#molecule\_type protein  
#residues 1-37 #label BUR  
#note this precursor was synthesized in a cell-free system directed by mRNA isolated from myeloma polyclones

REFERENCE A90373  
#authors McKean, D.; Potter, M.; Hood, L.  
#journal Biochemistry (1973) 12:749-759  
#title Mouse immunoglobulin chains. Partial amino acid sequence of a kappa chain.

#cross-references MUID:73140224  
#contents MOPC 321  
#accession A90373  
#molecule\_type protein  
#residues 21-132 #label MCK  
#note the partial sequence of the C region of this Bence Jones protein was also determined; it differs from that reported for mouse MOPC 21 only in the transposition of two nearby residues

REFERENCE A90374  
#authors McKean, D.; Potter, M.; Hood, L.  
#journal Biochemistry (1973) 12:760-771  
#title Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.

#cross-references MUID:73140225  
#contents TEPC 124  
#accession A90374  
#molecule\_type protein  
#residues 21-131 #label MC2  
#note the sequence is compatible with that of MOPC 321 except in having 47-Glx, 51-Trp, and 118-Ala

COMMENT The MOPC 321 sequence is shown.  
RESIDUES Residues 1-20 are the signal sequence.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

FEATURE 36-114  
#domain immunoglobulin homology #label IMM

SUMMARY #length 132 #molecular-weight 14523 #checksum 370

Query Match 85.6%; Score 806; DB 2; Length 132;  
Best Local Similarity 77.1%; Pred. No. 3.08e-75;

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Matches 101; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

Db 1 metdtllwllwpgsgdivltqspaslpmslqgratiscraeksvntynsfmzy 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:| 1:|:|:|  
Qy 1 MESDILLWLLWPGSGDIVLTQSPASLGVSGLQGRATISCRASKSVSTSGSYNMHWY 60

Db 61 zkpqzppklliyvaenlzagiparfsgsgertbftlnibpzyabdvatyczszbzbpw 120  
::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:| 1:|  
Qy 61 QQKPGQTPKLLIYASNTLESQVPARFSGSGGTFTLTIHPVEEDAAITYYCOHSRENPY 120

Db 121 tfgggtkleik 131  
|||||  
Qy 121 TFGGGTKLEIK 131

RESULT 5  
ENTRY PH1226 #type fragment  
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)  
ORGANISM #formal name Homo sapiens #common name man  
DATE 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 30-Apr-1995  
ACCESSIONS PH1226  
REFERENCE PH1224  
#authors Weissenborn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmueller, G.; Weidle, U.H.  
#journal Gene (1992) 121:271-278  
#title Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor.

#accession PH1226  
#molecule\_type mRNA  
#residues 1-131 #label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS immunoglobulin

FEATURE 1-20 #domain signal sequence #status predicted #label SIGV  
21-131 #product Ig light chain V region #status predicted #label MAT  
SUMMARY #length 131 #checksum 4648

Query Match 85.5%; Score 805; DB 5; Length 131;  
Best Local Similarity 85.5%; Pred. No. 4.01e-75;  
Matches 112; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Db 1 metdtllwllwpgsgdivltqspaslpmslqgratiscraekslidydgdsymwy 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:| 1:|:|:|  
Qy 1 MESDILLWLLWPGSGDIVLTQSPASLGVSGLQGRATISCRASKSVSTSGSYNMHWY 60

Db 61 qkpqzppklliyvaenlzagiparfsgsgertbftlnibpzyeedaatyycqssedpp 120  
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:| 1:|  
Qy 61 QQKPGQTPKLLIYASNTLESQVPARFSGSGGTFTLTIHPVEEDAAITYYCOHSRENPY 120

Db 121 tfgggtkleik 131  
|||||  
Qy 121 TFGGGTKLEIK 131

RESULT 6  
ENTRY JL0073 #type complete  
TITLE aberrant kappa transcript - mouse  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 21-Nov-1993 #sequence\_revision 21-Nov-1993 #text\_change 21-Nov-1993

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ACCESSIONS      JL0073
REFERENCE        Carroll, W.L.; Mendel, E.; Levy, S.
#authors         Mol. Immunol. (1988) 25:991-995
#journal         Hybridoma fusion cell lines contain an aberrant kappa
#title           transcript.
#cross-references MUID:89112230
#accession       JL0073
#status          preliminary
#residues        1-128 ##label CAR
SUMMARY          #length 128 #molecular-weight 14060 #checksum 5564

Query Match      83.3%; Score 785; DB 13; Length 128;
Best Local Similarity 93.2%; Pred. No. 7,84e-73;
Matches 109; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 1 metdtdllwvllwpqstgdivltgspaslavslqqratisytskvsstgysymhw 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVTSYGYMHY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 qkpgqprlliyvsnlesgvparsfgsgsgtdftlnihpveedaatyqcqhre 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 QQKPGQTPKLLIYLASNLESVPARFSGSGSGTDTLTINHPVEEDAATYYCQHSRE 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
ENTRY      S52448      #type complete
TITLE      Ig kappa chain V region - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       08-May-1995 #sequence_revision 21-Jul-1995 #text_change
          21-Jul-1995

ACCESSIONS      S52448
REFERENCE        Berdoz, J.; Kraehenbuhl, J.P.
#authors         Submission submitted to the EMBL Data Library, November 1994
#description      Specific amplification by the polymerase chain reaction of
                  rearranged genomic variable regions of immunoglobulin genes
                  from mouse hybridoma cells.
#accession       S52448
#status          preliminary
#molecule_type DNA
#residues        1-128 ##label BER
#cross-references EMBL:X82689

GENETICS
#introns        14/1
SUMMARY          #length 128 #molecular-weight 14020 #checksum 5468

Query Match      80.0%; Score 754; DB 11; Length 128;
Best Local Similarity 90.7%; Pred. No. 2,76e-69;
Matches 107; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 metdtdllwvlllfpqstgdivltgspaslavslqqratisytskvsstgysymhw 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 MESDTLLWVLLWV-PCSTGDIVLTQSPASLGVSIGQRATISCRASKSVTSYGYMHY 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 nqkpgqprlliyvsnlesgvparsfgsgsgtdftlnihpveedaatyqcqhre 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 YQKPGQTPKLLIYLASNLESVPARFSGSGSGTDTLTINHPVEEDAATYYCQHSRE 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
ENTRY      KWS84      #type complete
TITLE      Ig kappa chain V region (PC6684) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
```

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DATE            01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
          11-Aug-1995
ACCESSIONS      A01938
REFERENCE        A93204
#authors         Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal         Nature (1978) 276:785-790
#title           Rearrangement of genetic information may produce
                  immunoglobulin diversity.
#cross-references MUID:79073152
#accession       A01938
#molecule_type protein
#residues        1-111 ##label WEI
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE         16-94      #domain immunoglobulin homology #label IMM
                23-92      #disulfide bonds #status predicted
SUMMARY          #length 111 #molecular-weight 12039 #checksum 2467

Query Match      78.7%; Score 741; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 8,41e-68;
Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 divltgspaslavslqqratiscrasksvstgysymhwqkpgqpklliyasnles 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLGVSIGQRATISCRASKSVTSYGYMHYQKPGQTPKLLIYLASNLES 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 gvparsfgsgtdftlnihpveedaatyqcqhrelptfgggtkleik 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GVPARFSGSGTDTLTINHPVEEDAATYYCQHSRENPTFGGKTLEIK 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
ENTRY      KWS75      #type complete
TITLE      Ig kappa chain V region (PC7175) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
          30-Sep-1993

ACCESSIONS      B01938; A01938
REFERENCE        A93204
#authors         Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal         Nature (1978) 276:785-790
#title           Rearrangement of genetic information may produce
                  immunoglobulin diversity.
#cross-references MUID:79073152
#accession       B01938
#molecule_type protein
#residues        1-111 ##label WEI
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS        immunoglobulin
FEATURE         23-92      #disulfide bonds #status predicted
SUMMARY          #length 111 #molecular-weight 12010 #checksum 2086

Query Match      77.9%; Score 734; DB 2; Length 111;
Best Local Similarity 94.6%; Pred. No. 5,30e-67;
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 1 divltgspaslavslqqratiscrasksvstgysymhwqkpgqpklliyasnles 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLGVSIGQRATISCRASKSVTSYGYMHYQKPGQTPKLLIYLASNLES 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 gvparsfgsgtdftlnihpveedaatyqcqhrelptfgggtkleik 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GVPARFSGSGTDTLTINHPVEEDAATYYCQHSRENPTFGGKTLEIK 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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RESULT 10
ENTRY   KVMS40      #type complete
TITLE   Ig kappa chain V region (PC7940) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
30-Sep-1993

ACCESSIONS C01938; A01938
REFERENCE  A93204
#authors  Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal  Nature (1978) 276:785-790
#title    Rearrangement of genetic information may produce
          immunoglobulin diversity.
#cross-references MUID:79073152
#accession C01938
#molecule_type protein
#residues  1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      immunoglobulin
FEATURE
23-92         #disulfide_bonds #status predicted
SUMMARY       #length 111 #molecular_weight 12038 #checksum 2027

Query Match 77.0%; Score 725; DB 2; Length 111;
Best Local Similarity 93.7%; Pred. No. 5,63e-66;
Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 1 divltqspaslaqlgratiscrasksvafgysymhwycqgqppklliyasnlles 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 DIVLTQSPASLGVLGRATISCRASKSVTSYGYSMHWYQKPGQTPKLLIYASNLIES 80
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 gvparfsgsgtdftlnihpveeedavtyycqhereipltfgggtkleik 111
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 GVPARFSGSGTDFTLNIHPVEEEDAAITYYQHSRENPTYFGGGTKLEIK 131

RESULT 11
ENTRY   KVMS85      #type complete
TITLE   Ig kappa chain V regions (PC2485, PC4039) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
05-Apr-1995

ACCESSIONS A01939
REFERENCE  A93204
#authors  Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal  Nature (1978) 276:785-790
#title    Rearrangement of genetic information may produce
          immunoglobulin diversity.
#cross-references MUID:79073152
#accession A01939
#molecule_type protein
#residues  1-111 ##label WEI
#note     the PC2485 and PC4039 sequences are identical
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
23-92         #disulfide_bonds #status predicted
SUMMARY       #length 111 #molecular_weight 11986 #checksum 2226

Query Match 76.4%; Score 720; DB 2; Length 111;
Best Local Similarity 91.9%; Pred. No. 2.09e-65;
Matches 102; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 1 divltqspaslaqlgratiscrasksvetegysymhwycqgqppklliyasnlles 60
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Qy 21 DIVLTQSPASLGVLGRATISCRASKSVTSYGYSMHWYQKPGQTPKLLIYASNLIES 80
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 gvparfsgsgtdftlnihpveeedaaiycqhereipltfgggtkleik 111
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 GVPARFSGSGTDFTLNIHPVEEEDAAITYYQHSRENPTYFGGGTKLEIK 131
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
ENTRY   S45715      #type complete
TITLE   antigen-Fab VL - Pseudomonas aeruginosa
ORGANISM #formal_name Pseudomonas aeruginosa
DATE     10-Dec-1994 #sequence_revision 10-Dec-1994 #text_change
10-Dec-1994

ACCESSIONS S45715
REFERENCE  S45714
#authors  Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.;
          Ohtsuka, H.; Higuchi, A.; Nomura, N.; Noguchi, H.; Arata,
          Y.
#journal  FEBS Lett. (1994) 346:246-250
#title    Application of (13)C NMR spectroscopy to paratope mapping for
          larger antigen-Fab complexes.
#accession S45715
#status    preliminary
#residues  1-112 ##label KIM
SUMMARY   #length 112 #molecular_weight 12168 #checksum 6129

Query Match 75.7%; Score 713; DB 12; Length 112;
Best Local Similarity 91.0%; Pred. No. 1.31e-64;
Matches 101; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 1 divltqspaslaqlgratiscrasksvstgysymhwycqgqpprlliyasnlles 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 DIVLTQSPASLGVLGRATISCRASKSVTSYGYSMHWYQKPGQTPKLLIYASNLIES 80
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 gvparfsgsgtdftlnihpveeedaanyhcqhardipltfgggtkleik 111
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 GVPARFSGSGTDFTLNIHPVEEEDAAITYYQHSRENPTYFGGGTKLEIK 131
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
ENTRY   S06731      #type complete
TITLE   Ig kappa chain precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
12-Apr-1995

ACCESSIONS S06731
REFERENCE  S06731
#authors  Alaneh, A.; Weiss, S.
#journal  Eur. J. Immunol. (1989) 19:1961-1963
#title    Sequence and linkage of the V(kappa)21A and G germ-line gene
          segments in the mouse.
#cross-references MUID:90060210
#accession S06731
#status    preliminary
#molecule_type DNA
#residues  1-120 ##label ALA
#cross-references EMBL:X16955
GENETICS
#introns   18/1
#superfamily immunoglobulin V region; immunoglobulin homology
CLASSIFICATION #length 120 #molecular_weight 13029 #checksum 5418
SUMMARY

Query Match 75.1%; Score 707; DB 5; Length 120;
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Best Local Similarity 83.3%; Pred. No. 6.33e-64;  
Matches 100; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Db 1 mesdtllllwllwpggsgtdvlqtspaslavslqgratiscrasivesveyygtslmqw 60  
Qy 1 MESDTLLLVLLWVFG-STGDIVLTQSPASLGVLQGRATISCRASKSVSTSGSYMHM 59

Db 61 vqtkpqpkllyiaasnvesgparfsqsgtdftlnihpveedatmyfcqqsryp 120  
Qy 60 YQKPKQTPKLLIYLASNLESGVPRFSGSGTDFTLNIHPVEEDAAATYQCQHSRENP 119

RESULT 14

ENTRY S09963 #type fragment  
TITLE Ig kappa chain V-J region (103-7E) - mouse (fragment)  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 30-Sep-1993  
ACCESSIONS S09963  
REFERENCE S09955  
#authors Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.  
#journal Eur. J. Immunol. (1990) 20:771-777  
#title Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies from autoimmune NZB mice.  
#cross-references MUID:90269328  
#accession S09963  
#molecule\_type mRNA  
#residues 1-111 ##label REI  
##cross-references EMBL:X51851  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 111 #checksum 3824

Query Match 74.6%; Score 703; DB 5; Length 111;  
Best Local Similarity 90.2%; Pred. No. 1.81e-63;  
Matches 101; Conservative 6; Mismatches 3; Indels 2; Gaps 2;

Db 1 divltqspaslavslqgratiscrasvsgsyhmwqkpgqpklliky-asnle 59  
Qy 21 DIVLTQSPASLGVLQGRATISCRASKSVSTSGSYMHYQKPKQTPKLLI-YLASNLE 79

Db 60 sqvparfsqsgtdftlnihpveedatyycqhsweipytfgggtkkleik 111  
Qy 80 SQVPARFSGSGTDFTLNIHPVEEDAAATYQCQHSRENPYTFGGGKLEIK 131

RESULT 15

ENTRY S24288 #type complete  
TITLE Ig kappa chain V region (J528/32) - mouse  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995  
ACCESSIONS S24288  
REFERENCE S24287  
#authors Moncharmont, B.  
#submission submitted to the EMBL Data Library, September 1991  
#description Cloning and sequencing of the cDNA coding for the variable regions of the heavy and light chains of two monoclonal antibodies to the estrogen receptor.  
#accession S24288  
##status preliminary  
##molecule\_type mRNA  
##residues 1-110 ##label MON  
##cross-references EMBL:X62703

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12

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 110 #molecular-weight 12055 #checksum 9833

Query Match 74.4%; Score 701; DB 5; Length 110;  
Best Local Similarity 91.9%; Pred. No. 3.05e-63;  
Matches 102; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Db 1 digltspaslavslqgratiscrasvsgsyhmwqkpgqpprlliliyvsnlles 60  
Qy 21 DIVLTQSPASLGVLQGRATISCRASKSVSTSGSYMHYQKPKQTPKLLIYLASNLES 80

Db 61 gvparfsqsgtdftlnihpveedatyycqhsweipytfgggtkkleik 110  
Qy 81 GVPARFSGSGTDFTLNIHPVEEDAAATYQCQHSRENPYTFGGGKLEIK 131

Search completed: Mon Jul 8 08:28:44 1996  
Job time : 21 secs.







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5

```
RESULT 4
ID KV3S MOUSE STANDARD; PRT; 111 AA.
AC P01671;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7175).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79073152
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790 (1978).
DR PIR; B01938; KVM575.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; 66974 CN;
```

Query Match 77.9%; Score 734; DB 4; Length 111;  
Best Local Similarity 94.6%; Pred. No. 7.28e-139;  
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Db 1 divltqspaslavslqqratiscrasksvstsgysymhwqkpgqpklliyasles 60
Qy 21 DIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYMHYQKPGQTPKLLIYASLES 80
Db 61 gvpafegsgsgtdftlnihpveedaatyycqhsreplptfgagtkleik 111
Qy 81 GVPARESGSGTDFTLNIHPVEEDAATYTCQHSRENPTYFGGCTKLEIK 131
```

```
RESULT 5
ID KV3T MOUSE STANDARD; PRT; 111 AA.
AC P01672;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7940).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79073152
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790 (1978).
DR PIR; C01938; KVM540.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
```

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FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12038 MW; 69104 CN;
```

Query Match 77.0%; Score 725; DB 4; Length 111;  
Best Local Similarity 93.7%; Pred. No. 8.86e-137;  
Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```
Db 1 divltqspaslavslqqratiscrasksvstsgysymhwqkpgqpklliyasles 60
Qy 21 DIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYMHYQKPGQTPKLLIYASLES 80
Db 61 gvpafegsgsgtdftlnihpveedaatyycqhsreplptfgagtkleik 111
Qy 81 GVPARESGSGTDFTLNIHPVEEDAATYTCQHSRENPTYFGGCTKLEIK 131
```

```
RESULT 6
ID KV3U MOUSE STANDARD; PRT; 111 AA.
AC P01673;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 2485 AND PC 4039).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79073152
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790 (1978).
CC -!- THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.
DR PIR; A01939; KVM585.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11986 MW; 66852 CN;
```

Query Match 76.4%; Score 720; DB 4; Length 111;  
Best Local Similarity 91.9%; Pred. No. 1.27e-135;  
Matches 102; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Db 1 divltqspaslavslqqratiscrasksvstsgysymhwqkpgqpklliyasles 60
Qy 21 DIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYMHYQKPGQTPKLLIYASLES 80
Db 61 gvpafegsgsgtdftlnihpveedaatyycqhsreplptfgagtkleik 111
Qy 81 GVPARESGSGTDFTLNIHPVEEDAATYTCQHSRENPTYFGGCTKLEIK 131
```

RESULT 7

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```
ID KV3L MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (CHPC 101).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79012520
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVMSC1.
DR HSSP; P01679; IGBB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; 65196 CN;
```

Query Match 72.6%; Score 684; DB 4; Length 111;  
Best Local Similarity 86.5%; Pred. No. 2.67e-127;  
Matches 96; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

```
Db 1 divltqspaslavslqgratiscasgsvdytgsymnywqgkpklliyasnlles 60
Qy 21 DIVLTQSPASLGSLGRATISCRASKSVSTGYSYMHYQKPGQTPKLLIYASNLLES 80
```

```
Db 61 giparfsgsgtdftlnihpveedaatyccqnedpytfgggtkleik 111
Qy 81 GVPARESGSGTDFLTNIHPVEEDAATYCCQHSRENPTYFGGGTKLEIK 131
```

```
RESULT 8
ID KV3M MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7043).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79073152
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; A01937; KVM543.
DR HSSP; P01679; IGBB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
```

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FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 65350 CN;
```

Query Match 71.7%; Score 675; DB 4; Length 111;  
Best Local Similarity 85.6%; Pred. No. 3.18e-125;  
Matches 95; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

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Db 1 divltqspaslavslqgratiscasgsvdytgsymnywqgkpklliyasnlles 60
Qy 21 DIVLTQSPASLGSLGRATISCRASKSVSTGYSYMHYQKPGQTPKLLIYASNLLES 80
```

```
Db 61 giparfsgsgtdftlnihpveedaatyccqnedpytfgggtkleik 111
Qy 81 GVPARESGSGTDFLTNIHPVEEDAATYCCQHSRENPTYFGGGTKLEIK 131
```

```
RESULT 9
ID KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP ABPC 22, SEQUENCE.
RM 79012520
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
RN [2]
RP PC 9245, SEQUENCE.
RM 79073152
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
CC -!- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KVM546.
DR HSSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; 64631 CN;
```

Query Match 71.3%; Score 672; DB 4; Length 111;  
Best Local Similarity 83.8%; Pred. No. 1.56e-124;  
Matches 93; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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Db 1 nivltqspaslavslqgratiscasgsvdytgsymnywqgkpklliyasnlles 60
Qy 21 DIVLTQSPASLGSLGRATISCRASKSVSTGYSYMHYQKPGQTPKLLIYASNLLES 80
```

```
Db 61 gyparfsgsgtdftlnidpveadaatyccqnedpytfgggtkleik 111
```







Db 61 giparfsgsgsgtdftlnihpveedaatyychqs-edpwtfgsgtkleik 110  
:-:|||||:|||||:|||||:|-:|||||:  
Qy 81 GWPAFSGSGGTDFTLNHPVEEDAATYYCQHRENPYTFGGTGKLEIK 131

Search completed: Mon Jul 8 08:28:04 1996  
Job time : 12 secs.



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W P S R E D

(TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:29:02 1996; MasPar time 4.45 Seconds  
243.853 Million cell updates/sec

Tabular output not generated.

Title: >US-08-137-117B-25  
Description: (1-131) from US08137117B.pap  
Perfect Score: 942  
Sequence: 1 MESDPLLLWLLWLPVSGT.....CQHSRENPTFGGTYKLEIK 131

Scoring table: PAM 150  
Gap 11

Searched: 70887 seqs, 8282111 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq22

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14

Statistics: Mean 30.229; Variance 161.993; scale 0.187

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description	Pred. No.
1	942	100.0	131	6	R28668	p12-k2.	Anti-idiotypic antibody	1.32e-63
2	851	90.3	130	14	R74967	Mouse MAb 3B9 light c	6.43e-54	1.96e-56
3	819	86.9	132	13	R70189	Amino acids sequence	1.11e-53	6.43e-54
4	816	86.6	131	1	P90543	Anti-idiotypic antibody	3.93e-53	1.11e-53
5	809	85.9	146	14	R74966	Anti-CD4 antibody MT	8.10e-53	3.93e-53
6	805	85.5	131	6	R32123	Anti-Leu 3a light cha	3.44e-52	8.10e-53
7	797	84.6	131	1	R04132	p64-k4 protein produc	2.51e-51	3.44e-52
8	786	83.4	131	6	R29008	kappa light chain var	3.01e-51	2.51e-51
9	785	83.3	132	3	R10920	Antibody 4A2 light ch	6.20e-51	3.01e-51
10	781	82.9	131	6	R30891	Light chain variable	6.50e-50	6.20e-51
11	768	81.5	131	1	R05089	Mouse 4C10 anti-idiot	4.73e-49	6.50e-50
12	757	80.4	132	7	R37716			4.73e-49

	13	725	77.0	112	14	R80272	VL region from an ant	1.57e-46
14	716	76.0 <td>110</td> <td>11</td> <td>R60564</td> <td>Anti-carcinomaembryonic</td> <td>7.70e-46</td> <td>7.70e-46</td>	110	11	R60564	Anti-carcinomaembryonic	7.70e-46	7.70e-46
15	706	74.9 <td>112</td> <td>2</td> <td>R07456</td> <td>N-terminal sequence o</td> <td>4.67e-45</td> <td>4.67e-45</td>	112	2	R07456	N-terminal sequence o	4.67e-45	4.67e-45
16	702	74.5 <td>212</td> <td>10</td> <td>R52659</td> <td>Porphyran antibody li</td> <td>9.59e-45</td> <td>9.59e-45</td>	212	10	R52659	Porphyran antibody li	9.59e-45	9.59e-45
17	701	74.4	124	3	R15442	Light chain variable	1.15e-44	1.15e-44
18	696	73.9 <td>110</td> <td>14</td> <td>R74956</td> <td>Immunoglobulin light</td> <td>2.82e-44</td> <td>2.82e-44</td>	110	14	R74956	Immunoglobulin light	2.82e-44	2.82e-44
19	692	73.5 <td>110</td> <td>14</td> <td>R74957</td> <td>Immunoglobulin light</td> <td>5.80e-44</td> <td>5.80e-44</td>	110	14	R74957	Immunoglobulin light	5.80e-44	5.80e-44
20	687	72.9 <td>112</td> <td>14</td> <td>R75431</td> <td>Human thyroid stimula</td> <td>1.43e-43</td> <td>1.43e-43</td>	112	14	R75431	Human thyroid stimula	1.43e-43	1.43e-43
21	685	72.7	218	14	R75457	Mouse antibody FB3-2	2.04e-43	2.04e-43
22	685	72.7	218	14	R75457	Mouse antibody FB3-2	2.04e-43	2.04e-43
23	684	72.6 <td>111</td> <td>11</td> <td>R60528</td> <td>Light chain variable</td> <td>2.45e-43</td> <td>2.45e-43</td>	111	11	R60528	Light chain variable	2.45e-43	2.45e-43
24	683	72.5 <td>125</td> <td>3</td> <td>R15440</td> <td>Light chain variable</td> <td>2.93e-43</td> <td>2.93e-43</td>	125	3	R15440	Light chain variable	2.93e-43	2.93e-43
25	671	71.2 <td>111</td> <td>10</td> <td>R55123</td> <td>Mouse anti-HIV mu5.5</td> <td>2.53e-42</td> <td>2.53e-42</td>	111	10	R55123	Mouse anti-HIV mu5.5	2.53e-42	2.53e-42
26	671	71.2 <td>111</td> <td>11</td> <td>R60302</td> <td>Anti HIV antibody lig</td> <td>2.53e-42</td> <td>2.53e-42</td>	111	11	R60302	Anti HIV antibody lig	2.53e-42	2.53e-42
27	663	70.4 <td>111</td> <td>1</td> <td>P90541</td> <td>Immunoglobulin L chai</td> <td>1.07e-41</td> <td>1.07e-41</td>	111	1	P90541	Immunoglobulin L chai	1.07e-41	1.07e-41
28	650	69.0 <td>112</td> <td>14</td> <td>R79156</td> <td>Human IgE receptor-bi</td> <td>1.10e-40</td> <td>1.10e-40</td>	112	14	R79156	Human IgE receptor-bi	1.10e-40	1.10e-40
29	649	68.9 <td>112</td> <td>14</td> <td>R79158</td> <td>Human IgE receptor-bi</td> <td>1.32e-40</td> <td>1.32e-40</td>	112	14	R79158	Human IgE receptor-bi	1.32e-40	1.32e-40
30	646	68.6 <td>111</td> <td>6</td> <td>R33305</td> <td>MaE11 light chain.</td> <td>2.26e-40</td> <td>2.26e-40</td>	111	6	R33305	MaE11 light chain.	2.26e-40	2.26e-40
31	644	68.4 <td>111</td> <td>13</td> <td>R65172</td> <td>Murine NM-01 variable</td> <td>3.23e-40</td> <td>3.23e-40</td>	111	13	R65172	Murine NM-01 variable	3.23e-40	3.23e-40
32	642	68.2 <td>111</td> <td>9</td> <td>R47494</td> <td>Murine anti-CD18 Ab 6</td> <td>4.63e-40</td> <td>4.63e-40</td>	111	9	R47494	Murine anti-CD18 Ab 6	4.63e-40	4.63e-40
33	640	67.9 <td>112</td> <td>2</td> <td>R10539</td> <td>Chimeric MAB 9.2.27</td> <td>6.63e-40</td> <td>6.63e-40</td>	112	2	R10539	Chimeric MAB 9.2.27	6.63e-40	6.63e-40
34	637	67.6 <td>110</td> <td>10</td> <td>R60810</td> <td>Light chain variable</td> <td>1.14e-39</td> <td>1.14e-39</td>	110	10	R60810	Light chain variable	1.14e-39	1.14e-39
35	635	67.4 <td>112</td> <td>3</td> <td>R13089</td> <td>Murine 1B4 light chai</td> <td>1.63e-39</td> <td>1.63e-39</td>	112	3	R13089	Murine 1B4 light chai	1.63e-39	1.63e-39
36	632	67.1 <td>121</td> <td>9</td> <td>R48615</td> <td>Sequence of the monoc</td> <td>3.33e-39</td> <td>3.33e-39</td>	121	9	R48615	Sequence of the monoc	3.33e-39	3.33e-39
37	631	67.0 <td>121</td> <td>6</td> <td>R33346</td> <td>Anti-Tac light chain</td> <td>3.99e-39</td> <td>3.99e-39</td>	121	6	R33346	Anti-Tac light chain	3.99e-39	3.99e-39
38	630	66.9 <td>126</td> <td>2</td> <td>R06375</td> <td>Humanised anti-Tac an</td> <td>3.99e-39</td> <td>3.99e-39</td>	126	2	R06375	Humanised anti-Tac an	3.99e-39	3.99e-39
39	630	66.9 <td>126</td> <td>2</td> <td>R24108</td> <td>Humanised anti-Tac an</td> <td>3.99e-39</td> <td>3.99e-39</td>	126	2	R24108	Humanised anti-Tac an	3.99e-39	3.99e-39
40	629	66.8 <td>106</td> <td>6</td> <td>R33309</td> <td>MaE15 light chain.</td> <td>4.77e-39</td> <td>4.77e-39</td>	106	6	R33309	MaE15 light chain.	4.77e-39	4.77e-39
41	627	66.6 <td>112</td> <td>14</td> <td>R74955</td> <td>Immunoglobulin light</td> <td>6.83e-39</td> <td>6.83e-39</td>	112	14	R74955	Immunoglobulin light	6.83e-39	6.83e-39
42	627	66.6 <td>118</td> <td>14</td> <td>R74965</td> <td>Anti-idiotypic antibod</td> <td>6.83e-39</td> <td>6.83e-39</td>	118	14	R74965	Anti-idiotypic antibod	6.83e-39	6.83e-39
43	627	66.6 <td>120</td> <td>9</td> <td>R48618</td> <td>Sequence of the monoc</td> <td>8.17e-39</td> <td>8.17e-39</td>	120	9	R48618	Sequence of the monoc	8.17e-39	8.17e-39
44	626	66.5 <td>133</td> <td>10</td> <td>R59511</td> <td>Sequence of the light</td> <td>8.17e-39</td> <td>8.17e-39</td>	133	10	R59511	Sequence of the light	8.17e-39	8.17e-39
45	617	65.5 <td>120</td> <td>9</td> <td>R48620</td> <td>Sequence of the light</td> <td>4.10e-38</td> <td>4.10e-38</td>	120	9	R48620	Sequence of the light	4.10e-38	4.10e-38

## ALIGNMENTS

RESULT 1  
ID R28668 standard; Protein; 131 AA.  
AC R28668;  
DT 30-MAR-1993 (first entry)  
DE p12-k2.  
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;  
KW plasmid; p12-k2; p12-h2.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /note= "Signal peptide"  
FT Protein 21..131  
FT /note= "Mature peptide"  
PN W09219759-A.  
PD 12-NOV-1992.  
PF 25-APR-1992; J00544.  
PR 25-APR-1991; JP-095476.  
PR 19-FEB-1992; JP-032084.  
PA (CHUS ) CHUGAI SEIYAKU KK.  
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
DR WPI; 92-398882/48.  
DR N-PSDB; Q30753.  
PT Reconstituted human antibody to human interleukin-6 receptor -  
PT has low antigenicity and contains mouse V-region complementarity  
PT determining regions  
PS Disclosure; Page 118; 207pp; Japanese.

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CC The sequences given in R28668-69 were encoded by plasmid sequences  
 CC which were used in example to illustrate the production of a human  
 CC antibody which recognises human interleukin-6 receptor (IL-6R). The  
 CC antibody comprises light (L) chain and heavy (H) chain variable  
 CC regions which were derived from a mouse monoclonal antibody produced  
 CC from the hybridoma AUK12-20 which contained the plasmids p12-k2 and  
 CC p12-h2.  
 SQ Sequence 131 AA;

Query Match 100.0%; Score 942; DB 6; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 1.32e-63;  
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 mesdtllwllwvpgstgdivltqpaslgvslgqratisckasvstsgysymhw 60  
 QY 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYHWY 60  
 Db 61 qkqpgqtpklllylasnlesgvpafsgsgtdftlnihpveedaatyqcshrenpy 120  
 QY 61 QKQPGQTPKLLIYLASNLES GVPARFSGSGTDFTLNIHPVEEDAATYTCQHSRENPY 120  
 Db 121 tfgggtkleik 131  
 QY 121 TFGGGTKLEIK 131

RESULT 2

ID R74967 standard; Protein; 130 AA.  
 AC R74967;  
 DT 02-FEB-1996 (first entry)  
 DE Anti-idiotype antibody Idio20 clone 20KB1.  
 KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;  
 KW complementarity determining region.  
 OS Mus sp.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= signal\_peptide  
 FN J07101999-A.  
 PD 18-APR-1995.  
 PE 06-OCT-1993; 272950.  
 PR 06-OCT-1993; JP-272950.  
 PA (HAGI/) HAGIWARA Y.  
 DR WPI; 95-182987/24.  
 DR N-PSDB; Q90432.  
 PT Novel anti-idiotype antibody against a human anticancer monoclonal  
 PT antibody - and DNA sequences encoding the antibody, useful in  
 PT pharmacology, medicine and biochemical fields.  
 PS Example 5; Page 20; 28pp; Japanese.  
 CC R74960-R74969 are clones of the anti-idiotype antibodies Idio3, Idio17,  
 CC Idio20, Idio27 and Idio33 against a human anticancer monoclonal antibody.  
 CC These antibodies and DNA encoding them are useful in pharmacological,  
 CC medical and biochemical fields of research.  
 SQ Sequence 130 AA;

Query Match 90.3%; Score 851; DB 14; Length 130;  
 Best Local Similarity 90.1%; Pred. No. 1.96e-56;  
 Matches 118; Conservative 6; Mismatches 6; Indels 1; Gaps 1;  
 Db 1 metdtllwllwvpgstgdivltqpaslgvslgqratisckasvstsgysymhw 60  
 QY 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYHWY 60  
 Db 61 qkqpgqtpklllylasnlesgvpafsgsgtdftlnihpveedaatyqcshrenpy 120  
 QY 61 QKQPGQTPKLLIYLASNLES GVPARFSGSGTDFTLNIHPVEEDAATYTCQHSRENPY 120

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4

QY 61 QKQPGQTPKLLIYLASNLES GVPARFSGSGTDFTLNIHPVEEDAATYTCQHSRENPY 120  
 Db 120 tfgggtkleik 130  
 QY 121 TFGGGTKLEIK 131

RESULT 3

ID R70189 standard; Protein; 132 AA.  
 AC R70189;  
 DT 20-SEP-1995 (first entry)  
 DE Mouse Mab 3B9 light chain.  
 KW Chimeric antibody; humanized antibody; antibody engineering;  
 KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy.  
 OS Mus sp.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= Sig\_peptide  
 FT Region 44..58  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Region 74..80  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Region 113..121  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FN W09507301-A.  
 PD 16-MAR-1995.  
 PE 07-SEP-1994; U10308.  
 PR 07-SEP-1993; US-117366.  
 PR 14-OCT-1993; US-136783.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Gross MS, Holmes SD, Sylvester DR;  
 DR WPI; 95-123387/16.  
 DR N-PSDB; Q83490.  
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 PS Disclosure; Fig.1; 97pp; English.  
 CC Spleen cells from mice immunized with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only  
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 CC chains were cloned into pGEM/ff+ and transformed into E. coli  
 CC DH5-alpha. The clones were sequenced (Q83490-91), and used for  
 CC antibody engineering.  
 SQ Sequence 132 AA;

Query Match 86.9%; Score 819; DB 13; Length 132;  
 Best Local Similarity 87.0%; Pred. No. 6.43e-54;  
 Matches 114; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
 Db 1 metdtllwllwvpgstgdivltqpaslgvslgqratisckasvstsgysymhw 60  
 QY 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYHWY 60  
 Db 61 qkqpgqtpklllylasnlesgvpafsgsgtdftlnihpveedaatyqcshrenpy 120  
 QY 61 QKQPGQTPKLLIYLASNLES GVPARFSGSGTDFTLNIHPVEEDAATYTCQHSRENPY 120  
 Db 121 tfgggtkleik 131  
 QY 121 TFGGGTKLEIK 131

RESULT	4	
ID	P90543 standard; protein; 131 AA.	
AC	P90543;	
DT	20-OCT-1989 (first entry)	
DE	Amino acid sequence of a v chi region gene.	
KW	V cji region; immunoglobulin; L chain variable region; HIV.	
OS	Mus musculus	
PN	EP-327000-A.	
PD	09-AUG-1989.	
PF	30-JAN-1989; 101583.	
PR	30-JAN-1988; JP-20255.	
PR	08-JUL-1988; JP-171385.	
PT	The Chemo-Sero-Therapeutic Research Institute.	
PI	Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,	
PI	Takatsuki K;	
DR	WPI; 89-229050/32.	
DR	N-PSDB; N90495.	
PT	Chimeric anti-human immune virus antibodies - contg. mouse variable	
PT	regions and human constant regions for diagnosis, treatment and	
PT	prevention of AIDS	
PS	Disclosure; Fig 8; 33pp; English.	
CC	The sequence is encoded by a v chi region gene (see N90495).	
CC	The sequence from Asp 21 encodes the L chain variable region.	
SC	Sequence 131 AA;	

	Query Match	86.6%	Score 816;	DB 1;	Length 131;
	Best Local Similarity	85.5%;	Pred. No. 1.11e-53;	Mismatches 9;	Gaps 0;
	Matches 112;	Conservative	Indels		
D <b>b</b>	1 metdtlllwwlpvqsgtgdilvtqpaslawslggratiscaksqsvdyddsymwy	60    ::      1 MESDTLLLWVCSGCDIVLTQSPASISGLVSGQRATISCRAKSVTSYCYMHMY			
Qy					
D <b>b</b>	61 qdkgppklliyaanslesgiiparfsgsgsrtdftlnihpvveedaatyccgsnepadf	120   ::   ::   ::   :			
Qy	61 QOKPGGTPLKLLIYLANSNLESVPARFSGSGSGETFTLNHPVEEDAATYYCQRSNPY	120   :   :  :			
D <b>b</b>	121 tfsggtkleik	131    :			
Qy	121 TFGGTTKEIK	131    :			

RESULT	5	
ID	R74966 standard; Protein; 146 AA.	
AC	R74966;	
DT	02-FEB-1996 (first entry)	
DE	Anti-idiotypic antibody Id1o17 clone 17Kb1.	
KW	Antibody; cancer; COR; heavy chain; light chain; immunoglobulin;	
KW	complementarity determining region.	
OS	Mus sp.	
FH	Key	Location/Qualifiers
FT	Peptide	1..13
FT	/label= signal_peptide	
PN	J07101999-A.	
PD	18-APR-1995.	
PF	06-OCT-1993; 217950.	
PR	06-OCT-1993; JP-272950.	
PA	(HAGI/) HAGIWARA Y.	
DR	WPI; 95-182987/24.	
DR	N-PSDB; Q90431.	
PT	Novel anti-idiotypic antibody against a human anticancer monoclonal	
FT	antibody - and DNA sequences encoding the antibody, useful in	

PT Pharmacology, medicine and biochemical fields.  
PS Example 5; Page 19, 28pp; Japanese.  
CC R74960-R74969 are clones of the anti-idiotypic antibodies Id103, Id107, Id1020, Id1021 and Id1033 against a human anticancer monoclonal antibody.  
CC These antibodies and DNA encoding them are useful in pharmacological, medical and biochemical fields of research.  
SQ Sequence 146 AA;

Query Match 85.9%; Score 809; DB 14; Length 146;  
Best Local Similarity 91.1%; Pred. No. 3.93e-53;  
Matches 113; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

[illegible]

Db 120 leik 123  
128 LEIK 131

## RESULT 6

RESOL. 0  
ID R32123 standard; Protein; 131 AA.  
AC R32123;  
DT 02-JUN-1993 (first entry)  
DE Anti-CD4 antibody WT 3.10 light chain variable region.  
KW immunosuppression; tissue transplantation; graft; L chain; V region;  
T-helper cell inhibition; transplant rejection; MAH;  
interleukin-2 receptor.

FH	Key	Location/Qualifiers
FT	Peptide	1.20

FT	Peptide	/label= signal	1..20
FT			
FT			21..120

```
FT region
FT /label= Variable
```

FI	/label= variable	121..131
FT	Region	

```
ET region
ET /label= J1
```

PN DE4143214-A.

PD 28-JAN-1993;  
DE414JZ14-A;

FD 28-0AN-1993.  
PF 30-DEC-1991; 143214.

PR 25--JUL-1991; DE-124759.

PR 30-DEC-1991; DE-143214.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Kaluza B, Riethmueller G, Scheuer W, Weidle U;

DR WPI; 93-037582/

DR N-PSDB; Q36609.

PT Synergistic antibody compn. for use as immunosuppressant -

PT comprises monoclonal anti-CD4 antibody

PT alpha- or anti-IL2R beta antibodies

PS Claim 5; Page 11; 18pp; German.

CC This sequence is the light chain

CC anti-CD4 monoclonal antibody fo

CC composition. MAb MT 3.10 is dep

CC 90090702). The anti-CD4 antibody

CC alpha or beta antibody. Individual

CC inhibiting and when used together

CC are improved; they synergistically

CC proliferation to effectively in

CC doses without significantly red

CC See also Q36608-Q36616.

SQ Sequence 131 AA;

```
Query Match      85.5%; Score 805; DB 6; Length 131;
Best Local Similarity 85.5%; Pred. No. 8.10e-53;
Matches 112; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
```

Dbb1 metdtllwlllwpqstgdvltgpaelpmslgqratisckasqldydgsymwy 60  
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
1 MESDTLLWLLLVPGSTGDVLTQSPASISGLVSLGQRATISCRASKSVTSGSYMHY 60

Dbb61 qdkpgppklliyaanslesigparfsgsqgtfdtlnihpveedaatyycqsedpp 120  
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
61 QDRFGQTPLLIIYASNLESIGPARFSGSGGTFTLNHPVEEDATYYCQSRENPY 120

Qyb121 tfgggtkleik 131  
|||||||  
Qy121 TFGGKTLEIK 131

RESULT 7

ID R04132 standard; protein; 131 AA.  
AC R04132;  
DT 06-SEP-1990 (first entry)  
DE Anti-Leu 3a light chain variable region gene product, 206 Vx.  
KW HIV; AIDS; anti-Leu3A; vaccine; ds.  
OS Mus musculus.  
PN EP-365209-A.  
PD PD 25-APR-1990.  
PF PF 11-OCT-1989; 010415.  
PR PR 17-OCT-1988; US-260558.  
PA (BECT) Becton Dickinson Co.  
PI Hinton R, Oi VT;  
DR WPI; 90-126329/17.  
DR N-P5DB; Q04039.  
PT New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
PS Claim 1; Fig 2; l2pp; English.  
CC Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV.  
SQ Sequence 131 AA;

Query Match 84.6%; Score 797; DB 1; Length 131;  
Best Local Similarity 84.0%; Pred. No. 3.44e-52;  
Matches 110; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Db	1	metdtllwllllwvpgstgdiultqpapaelavslqgraticskasqevdydgdsymnw	60
		:	
		:	
Qy	1	MESDTLLWLLLLWVPGSTGDIULTQPASGLVSLGQRATISCRASKSVSTSGSYMHY	60
		:	
		:	
Db	61	qkpgqpklliyaaanlesgiparfctgsqsgtdftlnihpveeedtatyyvcqsgyedpp	120
Qy	61	QKPGQKPKLLIYLASNLESQVPARFSGSGSGTDTFLNIHPVEEDATYYCQHSRENPY	120
Db	121	tfaggtlnleik	131
		:	
Qy	121	TFGGTKLEIK	131
		:	
RESULT	8		
ID	R29008	standard; Protein; 131 AA.	
AC	R29008;		
DT	30-MAR-1993	(first entry)	
DE	p64-k4 protein product.		
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;		

KW	heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
KS	plasmid; p64-k4; p64-h2.
Q8	Synthetic.
FH	Key Location/Qualifiers
FT	Peptide I..20
FT	/note= "Signal peptide"
FT	Protein 21...131
FT	/note= "Mature peptide"
PV	WO9219759-A.
PD	12-NOV-1992.
PF	24-APR-1992; J00544.
PR	25-APR-1991; JP-095476.
PT	19-FEB-1992; JP-032084.
PA	(CHUS) CHUGAI SEIYAKU KK.
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR	WPI; 92-398882/48.
NF	N-P5DB; Q30757.
PT	Reconstituted human antibody to human interleukin-6 receptor -
PT	has low antigenicity and contains mouse V-region complementarity
PT	determining regions
PS	Disclosure; Page 124-125; 207pp; Japanese.
CC	The sequences given in R29008-09 were encoded by plasmids which were
CC	used in example to illustrate the production of a human antibody which
CC	recognises human interleukin-6 receptor (IL-6R). The antibody
CC	comprises light (L) chain and heavy (H) chain variable regions which
CC	were derived from a mouse monoclonal antibody produced from the
CC	hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2.
SQ	Sequence 131 AA;
<hr/>	
Query Match	83.4%; Score 786; DB 6; Length 131;
Best Local Similarity	82.4%; Pred. No. 2.51e-51;
Matches 108; Conservative 10; Mismatches 13; Indels 0; Gaps 0;	
Dc	1 mesdtlllwlwvpgstgdiivilqspaslavslqrqtatiscrasesvdsgnsfmhw 60       :       :       :       :       :       :   :
Qy	1 WESDTLLWLWWPGSGTGVLTQTSPASLVGSLGRATISCRASKSVTSVCYSVMHW 60       :       :       :       :       :       :   :
Dc	61 gkbpqpkklliyrasnlesigiparfsgsgsrtdftlnpveadadvayycqsndpp 120       :       :       :       :       :       :   :
Qy	61 QQKPEQTPKLLIIYASNLESIGVPARFSGSGSGTDFTLNHPVEEDAAYTCQSRENPY 120       :       :       :       :       :       :   :
Dc	121 tfgagtklelk 131       :       :
Qy	121 TFGGTKLEIK 131       :       :

RESULT	9	
ID	R10920 standard; Protein; 132 AA.	
AC	R10920;	
DT	08-MAY-1991 (first entry)	
DE	kappa light chain variable region of T84.66 monoclonal antibody.	
KW	MAB T84.66; kappa light chain; carcinoembryonic antigen; CEA;	
KW	human adenocarcinoma; mouse-human chimaeeric antibody.	
OS	Mus musculus.	
FR	Key	Location/Qualifiers
FT	Peptide	21..38
FT	/label=	tryptic peptide
FT	/note=	"sequenced as peptide fragment"
FT	Region	44..57
FT	/label=	complementarity determining region
FT	Region	70..80
FT	/label=	complementarity determining region
FT	Region	110..121
FT	/label=	complementarity determining region

PN W09101990-A.  
PD 21-FEB-1991.  
PF 19-JUL-1990; U004049.  
PR 26-JUL-1989; US-385102.  
PI (CITY ) CITY OF HOPE.  
PA Shively JE, Riggs AD, Neumaier M;  
DR WPI; 91-073486/10.  
DR N-PSDB; Q10834.  
PT Novel anti-CEA antibody - comparable to ATCC Accession No. BH  
PT 8747, produced by recombinant DNA, used in diagnosis of tumours  
PS Claim 4; Page 18; 24pp; English.  
CC The light chain variable region of murine MAb 84.66 was cloned and  
CC sequenced. It was used to produce mouse V-human C antibodies with high  
CC affinity for CEA. Chimeric murine-human anti-CEA Abs are used to  
CC diagnose human colon adenocarcinomas.  
CC See also Q11098 and Q10835-Q10848.  
SQ Sequence 132 AA;

Query Match 83.3%; Score 785; DB 3; Length 132;  
Best Local Similarity 79.4%; Pred. No. 3.01e-51;  
Matches 104; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

Db 1 metdtllllwllwpgstgdivltqspaslavslqgratmscrageavdvgvflhw 60  
||:|||||  
QY 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLVSLGQRATISCRASKSVTSYGMHWY 60  
|||||  
Db 61 qkqpggpklliyasnesgipvfsgtqrtdtliidpveaddvatycqgtneqpy 120  
|||||  
QY 61 QKPGQTPKLLIYLASNLESGVPARFSGSGGTDTLNIHPVEEDAATYYCQHSRENPY 120  
|||||

Db 121 tfgggtkleik 131  
|||||

QY 121 TFGGGTKLEIK 131

## RESULT 10

ID R30881 standard; Protein; 131 AA.  
AC R30881;  
DT 10-MAY-1993 (first entry)  
DE Antibody 4A2 light chain constant region.  
KW Fd'; fragment; human; 4A2; constant region; Fab'; F(ab')2; antibody;  
KW light chain; primer.  
OS Mus musculus.  
PN W09222324-A.  
PD 23-DEC-1992.  
PF 15-JUN-1992; U004976.  
PR 14-JUN-1991; US-714175.  
PA (XOMA ) XOMA CORP.  
PI Better MD, Carroll S, Horwitz AH;  
DR WPI; 93-017909/02.  
DR P-PSDB; Q34575.  
PT Polynucleotide sequences encoding Fab' and F(ab')2 fragments -  
PT used to produce, e.g. antibody-ricin A chain immuno:toxin(s)  
PS Disclosure; Fig 10; 92pp; English.  
CC This sequence represents the light chain constant domain (CL) from  
CC mouse antibody 4A2. This sequence was used in conjunction  
CC with the Fd' sequences given in Q34567-72 to produce chimeric Fd'  
CC vectors.  
SQ Sequence 131 AA;

Query Match 82.9%; Score 781; DB 6; Length 131;  
Best Local Similarity 84.0%; Pred. No. 6.20e-51;  
Matches 110; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Db 1 nesdtllllwllwpgstgdivltqspaslavslqgratmscrageavdvgvflhw 60  
|||||  
QY 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLVSLGQRATISCRASKSVTSYGMHWY 60  
|||||  
Db 61 qkqpggpklliyasnesgipvfsgtqrtdtliidpveaddvatycqgtneqpy 120  
|||||  
QY 61 QKPGQTPKLLIYLASNLESGVPARFSGSGGTDTLNIHPVEEDAATYYCQHSRENPY 120  
|||||  
Db 121 tfgggtkleik 131  
|||||  
QY 121 TFGGGTKLEIK 131

## RESULT 11

ID R05089 standard; protein; 131 AA.  
AC R05089;  
DT 04-OCT-1990 (first entry)  
DE Light chain variable domain of human chorion gonadotropin-binding peptd.  
KW Human chorionic gonadotropin; antibodies; choriocarcinoma; abortion;  
KW tumour detection; complementary determining regions;  
KW pregnancy prevention; light chain.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT Binding-site 44..58  
FT /label=CDR 74..80  
FT Binding-site 113..120  
FT /label=CDR  
PN EP-370581-A.  
PD 30-MAY-1990.  
PF 21-NOV-1989; 202951.  
PR 25-NOV-1988; NL-002902.  
PA (ALKU) AKZO NV.  
PI van Wezenbeek PM;  
DR WPI; 90-165307/22.  
DR N-PSDB; Q04694.  
PT Polypeptide(s) which specifically bind human chorionic gonadotropin -  
PT contg. antigen-binding domains comprising complementary  
PT determining domains.  
PS Disclosure; P; English.  
CC Together with the heavy chain variable domain (R05090) the sequence forms  
CC a hCG-binding antibody fragment (FhCG). For the production of Abs  
CC the variable region was fused to a constant region of human origin.  
CC The product can be used to prevent pregnancy or for combatting  
CC choriocarcinomas or other hCG-producing tumours.  
CC They also have diagnostic applications as immune reagents for in vivo  
CC diagnosis, eg for localisation of tumours and for in vitro diagnosis for  
CC detection of hCG in body fluids.  
SQ Sequence 131 AA;

Query Match 81.5%; Score 768; DB 1; Length 131;  
Best Local Similarity 79.4%; Pred. No. 6.50e-50;  
Matches 104; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

Db 1 mekdtllllwllwpgstgdivltqspaslavslqgratmscrageavdvgvflhw 60  
|||||  
QY 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLVSLGQRATISCRASKSVTSYGMHWY 60  
|||||

Db 61 qkqpggpklliyasnesgipvfsgtqrtdtliidpveaddvatycqgtneqpy 120  
|||||

QY 61 QKPGQTPKLLIYLASNLESGVPARFSGSGGTDTLNIHPVEEDAATYYCQHSRENPY 120  
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Db 121 tfgggtkleik 131

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QY 121 TFGGCTKLEIK 131
|||||
RESULT 12
ID R37716 standard; Protein; 132 AA.
AC R37716;
DT 30-SEP-1993 (first entry)
DE Mouse 4C10 anti-idiotypic Ab light chain V region.
KW MAIA; monoclonal antibody; hybridoma; organ transplant rejection;
KW immuno-modulator; cancer; treatment; diagnosis; melanoma;
KW anti-cancer immunity; enhancement; suppression.
OS Mus musculus.
FH Key Location/Qualifiers
FT Misc_difference 31
FT /note= "Thr -> Ser, from PCR substituted gene"
PN W09310221-A.
PD 27-MAY-1993.
PF 12-NOV-1992; U10166.
PR 13-NOV-1991; US-791934.
PA (REGC ) UNIV CALIFORNIA.
PI Hastings A, Irie RF, Morrison SL.
DR WPI; 93-182538/22.
PT Chimeric murine-human anti-idiotypic monoclonal antibodies -
PT useful as immuno-modulators for treating and diagnosing cancers,
PT and for suppressing organ transplant rejection and auto-immune
PT diseases
PS Disclosure; Page 30-31; 46pp; English.
CC The sequence is that of the 4C10 anti-idiotypic Ab light chain V region
CC which was used in the construction of a murine/human monoclonal
CC anti-idiotypic antibody (MAIA). The MAIA elicits an anti-ganglioside
CC response and produces antibodies which induce cytotoxic destruction
CC of cancer cells bearing the gangliosides. It can be used for treating
CC cancers partic. melanomas. It can also be used as an immunomodulator to
CC enhance anti-cancer immunity, suppress organ transplant rejection and
CC suppress auto-immune disease. The MAIA can also be used in the diagnosis
CC of cancers.
SQ Sequence 132 AA;

Query Match 80.4%; Score 757; DB 7; Length 132;
Best Local Similarity 79.5%; Pred. No. 4.73e-49;
Matches 105; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

Db 1 metdltllwllwvpgtgdvltqspaelavslqgratmscraseavdsvnsmfhw 60
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QY 1 MESDTLLWLLWVPGTGDVLTQSPASLGVSIGQRATISCRASKSVSTSGSYMHY 60

Db 61 qkbpqppklllyrasklegiparfsgseardftltinpveadvatvycqgnedpt 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 QQKPGQTPKLLIYASLNLESQVPAFSGSGGDTFTLNHPVEEDAATYYCQHSRNP- 119
|||||

Db 121 wtfgggwklek 132
|||||
QY 120 YTFGGGCTKLEIK 131

RESULT 13
ID R80272 standard; Protein; 112 AA.
AC R80272;
DT 27-FEB-1996 (first entry)
DE V1 region from an antibody against cancer-specific mucin.
KW Antibody; heavy chain; light chain; variable region; cancer; mucin;
KW hybridoma cell; murine; mouse; pancreatic cancer cell; expression vector;
KW Fv; human; constant domain; chimera; anaphylaxis.

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OS Synthetic.
FH Key Location/Qualifiers
FT Domain 24..38
FT /label= CDR1
FT Domain 54..60
FT /label= CDR2
FT Misc_difference 64
FT /note= "encoded by GAG"
FT Domain 93..101
FT /label= CDR3
PN FR2714915-A1.
PD 13-JUL-1995.
PF 13-JAN-1994; JP-002131.
PR (TOX) ) TOSOH CORP.
PI Chung Y, Iba Y, Kaneko T, Sowa M, Yasukawa K;
DR WPI; 95-247908/33.
DR N-PSDB; Q98534.
PT New variable domains of antibody recognising cancer specific mucin
PT - and related DNA and expression vectors, producing chimeric
PT mouse-human antibody for diagnosis and treatment of cancer
PS Claim 6; Page 16-17; 25pp; French.
CC The amino acid sequence of the variable region from the light chain of an
CC antibody against cancer-specific mucin. The coding sequence was isolated
CC from M2 hybridoma cells expressing a murine antibody reactive with
CC pancreatic cancer cells. The DNA encoding the antibody variable regions
CC from the heavy (Q98533) and light chains were isolated and inserted into
CC vectors. These vectors express the domains as an Fv antibody. Vectors
CC which additionally contain genes encoding the human constant domains
CC express a chimeric mouse-human antibody. The antibodies are useful in
CC the detection and treatment of cancer. The chimeras should be less likely
CC to cause anaphylaxis than the original murine antibody.
SQ Sequence 112 AA;

Query Match 77.0%; Score 725; DB 14; Length 112;
Best Local Similarity 91.9%; Pred. No. 1.52e-46;
Matches 102; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db 1 divltqspaslavslqgratiscrasksvstsfaymhwqkpgqppklllylasnles 60
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QY 21 DIVLTQSPASLGVSIGQRATISCRASKSVSTSGSYMHYQKPGQTPKLLIYASLNLES 80
|||||

Db 61 gvpdrfsgsgtdftlnhpveeedaatyycqhsrefpwtfgggtkleik 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 81 GVPARFSGSGGDTFTLNHPVEEDAATYYCQHSRNPYTFGGGCTKLEIK 131
|||||

RESULT 14
ID R60564 standard; Protein; 110 AA.
AC R60564;
DT 25-APR-1995 (first entry)
DE Anti-carcinoembryonic antigen chimeric light chain Ab.
KW Anti-carcinoembryonic antigen chimeric antibodies; CEAS;
KW chimeric human-murine; breast or colorectal carcinoma;
KW light chain.
OS Chimeric Mus muscaris.
OS Chimeric Homo sapiens.
PN W09419466-A.
PD 01-SEP-1994.
PF 16-FEB-1994; U01709.
PR 16-FEB-1993; US-017570.
PA (DOWC ) DOW CHEM CO.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Goullie BB, Kaplan DA, Mezes PS, Rixon MM, Schlom J;

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Search completed: Mon Jul 8 08:29:28 1996  
Job time : 26 secs.



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WAP5RL4 (TM)

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:38:26 1996; MacPar time 279.00 Seconds

Tabular output not generated. 1027.715 Million cell updates/sec

Title: >US-08-137-117B-26

Description: (1-405) from US08137117B.seq

Perfect Score: 405

N.A. Sequence: 1 ATGGGATGGAGCGGATCTT.....CTCTGTCACATGCTCTGCA 405

Comp: TACCTTACTCTGCCCTAGAA.....GAGACGATGACAGACGT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 264399 seqs, 353985056 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

emb1-new11

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN

9:PRI1 10:PRI2 11:PRI3 12:PRO1 13:PRO2 14:ROD 15:SYN

16:UNC 17:VRT 18:VIR

genbank91

19:BCT1 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7

26:INV1 27:INV2 28:INV3 29:INV4 30:INV5 31:MAM1 32:MAM2

33:PAT1 34:PAT2 35:PAT3 36:PHG 37:PLN1 38:PLN2 39:PLN3

40:PLN4 41:PLN5 42:PLN6 43:PLN7 44:PRI1 45:PRI2 46:PRI3

47:PRI4 48:PRI5 49:PRI6 50:PRI7 51:PRI8 52:PRI9 53:ROD1

54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD6 59:ROD7 60:STR

61:SYN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5

68:VRL6 69:VRT1 70:VRT2 71:VRT3

genbank-new11

72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN

79:PRI1 80:PRI2 81:PRI3 82:ROD 83:STR 84:SYN 85:UNA

86:VRL 87:VRT

u-emb144\_91

88:part1

Statistics: Mean 10.395; Variance 4.346; scale 2.392

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	312	77.0	462	56	MUSIGKCLS	Mouse IgMk rearranged 4.07e-274
2	307	75.8	405	56	MUSIGHM195	Mus musculus Ig heavy 4.32e-269
3	296	73.1	421	59	S51851	M104E myeloma immunog 4.83e-258
4	292	72.1	440	55	MUSHA5	Mouse active H-chain 4.99e-254
5	286	70.6	291	56	MUSIGHZ2H	Mouse Ig germline hea 5.20e-248
6	285	70.4	440	55	MUSHA3	Mouse active H-chain 5.23e-247
7	284	70.1	440	55	MUSHA6	Mouse Ig active H-chain 5.25e-246
8	283	69.9	408	56	MUSIGHFV	Mouse Ig active alpha 5.28e-245
9	282	69.6	348	53	MDICMVAU	M.domesticus IgM vari 5.31e-244
10	281	69.4	440	55	MUSHA4	Mouse active H-chain 5.33e-243
11	279	68.9	450	33	A07953	Artificial sequence f 5.37e-241
12	278	68.6	348	53	MDICMVBG	M.domesticus IgM vari 5.39e-240
13	278	68.6	2908	56	MUSIGHZ2F	Mouse Ig rearranged h 5.39e-240
14	273	67.4	412	56	MUSIGHFX	Mouse Ig family J558 5.47e-235
15	273	67.4	414	35	I05341	Sequence 3 from paten 5.47e-235
16	273	67.4	414	56	MUSIGGAJB	Mouse Ig gamma active 5.47e-235
17	272	67.2	348	55	MUSANTDNAM	Mouse anti-DNA antibo 5.48e-234
18	272	67.2	547	56	MUSICHAPA	Mouse Ig rearranged H 5.48e-234
19	270	66.7	429	56	MUSIGGV8	Mus musculus anti-HIV 5.49e-232
20	270	66.7	484	56	MUSIGH4C11	Mouse IgH chain mRNA, 5.49e-232
21	270	66.7	490	56	MUSIG4C11A	Mouse anti-idotype im 5.49e-232
22	267	65.9	451	55	MUSANTVDJ	Mouse anti-DNA autoan 5.50e-229
23	267	65.9	588	34	A23165	Artificial construct 5.50e-229
24	267	65.9	588	56	MUSIGGVAZ	Mus musculus IgG chai 5.50e-229
25	266	65.7	411	56	MUSIGHFY	Mouse Ig family J558 5.49e-228
26	265	65.4	342	56	MUSIGHADY	Mouse Ig heavy-chain 5.49e-227
27	265	65.4	352	53	MMIGIKH3	Mouse mRNA fragment f 5.49e-227
28	265	65.4	414	56	MUSIHCB	Mus musculus immunogl 5.49e-227
29	265	65.4	462	56	MUSIGHXZ	Mouse Ig rearranged g 5.49e-227
30	264	65.2	352	53	MMIGIKH4	Mouse mRNA fragment f 5.49e-226
31	263	64.9	474	54	MMAB1G3	M.musculus Mab 1G3 mR 5.48e-225
32	262	64.7	601	56	MUSIGHVA	Mouse Ig unrearranged 5.47e-224
33	261	64.4	351	59	S54755	IgG3 VH-anti-DNA IgG3 5.46e-223
34	261	64.4	509	56	MUSIGHAAG	Mouse Ig rearranged g 5.46e-223
35	260	64.2	454	53	MMIGHVDJ	M.musculus mRNA for i 5.45e-222
36	259	64.0	354	53	MMBV1619H	M.musculus heavy chai 5.43e-221
37	259	64.0	653	54	MMIGHV9	Mouse germline immuno 5.43e-221
38	259	64.0	767	56	MUSIGHVK2	Mouse Ig germline H-c 5.43e-221
39	258	63.7	352	54	MMIGHVR1	Mouse mRNA fragment f 5.42e-220
40	258	63.7	383	55	MMU28805	Mus musculus MoAb Mc3 5.42e-220
41	258	63.7	401	56	MUSIGKXE	Mouse Ig active gamma 5.42e-220
42	258	63.7	508	56	MUSIGF63A	Mouse anti-idotype im 5.42e-220
43	258	63.7	821	55	MMU26990	Mus musculus, isolate 5.42e-220
44	258	63.7	871	14	MM26990	Mus musculus, isolate 5.42e-220
45	258	63.7	1518	56	MUSIGAZA	Mouse Ig rearranged g 5.42e-220

## ALIGNMENTS

RESULT 1  
LOCUS MUSIGKCLS 462 bp mRNA ROD 15-MAR-1989  
DEFINITION Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J)  
anti-DNA\_autoantibody.  
ACCESSION M20831  
KEYWORDS V-region; autoantibody; immunoglobulin heavy chain.  
SOURCE Mouse (strain (NZBXW)F-1) spleen hybridoma cell line BXW-DNA16,  
cDNA to mRNA.  
ORGANISM Mus musculus





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Db 273 cagaagtccaagggcaaggccacattgactgtagacaaatctccacagcactacatg 332
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 CAGAAATTCAGGGCAAGCCACATTCAGTGTGACAAATCTCCAGCACGCCCTACATG 300

Db 333 cagctcaacagcctgacatctgaggaactctgcagctctattactgtgcaagagatagtaac 392
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 CATCTCAGCAGCCTGACATCTCAGGACTCTGCAGTCTATTACTGTGCAAGGGGGGTTAAC 360

Db 393 tactactttgactactggggccaaggcaccactctcacagcttc 436
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 361 --CG-CTTTGCTTACTGGGGCAAGGCACTCTGCTCCTGCTC 401

RESULT 5
LOCUS MUSIGH2H 2911 bp DNA ROD 25-JUL-1991
DEFINITION Mouse Ig germline heavy chain gene V-D-J region, hybridoma
ACCESSION V0205.12.
KEYWORDS V-region; germline; immunoglobulin heavy chain.
SOURCE Mouse DNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 2911)
AUTHORS Both,G.W., Taylor,L., Pollard,J.W. and Steele,E.J.
TITLE Distribution of mutations around rearranged heavy-chain antibody
variable-region genes
JOURNAL Mol. Cell. Biol. 10, 5187-5196 (1990)
MEDLINE 90377208
COMMENT NCBI gi: 196348
FEATURES
source 1..2911
/organism="Mus musculus"
/strain="C57BL/6J"
/sub_species="domesticus"
/sequenced_mol="DNA"

BASE COUNT 828 a 557 c 675 g 851 t
ORIGIN

Query Match 70.6%; Score 286; DB 56; Length 2911;
Best Local Similarity 91.2%; Pred. No. 5,20e-249;
Matches 333; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

Db 759 caggtgtcctctcaggtccagctgcaacaatctggacctgagctggtgaagcctggg 818
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 44 CAGGTGTCCACTCTCAGATCCAGCTGCAGCACTCTGCACCTGAGCTGATGAGCCTGGG 103

Db 819 cttcagtgagatattctgtgaagctcttgatacacgcttcactgactactacatgaact 878
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Qy 104 CTTCAGTGAAGATATCTCGAAGGCTTCTGGTTACTCATTCACTAGCTATTACATCACT 163

Db 879 gggtagagcagagccatggaagagccttgagtgagattgaagattatcctcaacaatg 938
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Qy 164 GGGTCAAGCAGAGGCCATCGAAAGAGCCCTGAGTGGATTGGATATATTGCTCTTCAATG 223

Db 939 gtggtactagctacaaccagaagttcaaggccaagccacattgactgtgacagaagtcct 998
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Qy 224 GTGTTACTAGCTACAAACAGAAATTCAGGGCAAGGCCACATTGACTGTTGACAAATCTT 283

Db 999 ccagcacagcctacatggagctccgcagcctgacatctgaggaactctgcagctcttact 1058
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Qy 284 CCAGCACAGCCTACATCTCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACT 343
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```
Db 1059 gtcaagaggggattacactggtttccttactggggccaagggaactctgtgactgtct 1118
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 344 CTCGAAGGGGGG--TA-ACGCTTTTGTCTTACTGGGGCAAGGCACTCTGGTCACTGTCT 400

Db 1119 ctgca 1123
|||||
Qy 401 CTCGA 405

RESULT 6
LOCUS MUSH3 440 bp mRNA ROD 24-JUL-1991
DEFINITION Mouse active H-chain VJ region, 5' cds.
ACCESSION M73330
KEYWORDS V-region; immunoglobulin heavy chain.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 440)
AUTHORS Rueff-Juy,D., Marche,P.N., Drapier,A.-M. and Cazenave,P.-A.
TITLE Junctional diversity of H and L chains allows the coexpression of
two mutually exclusive idiotopes (Id1104 and Id1558)
JOURNAL J. Immunol. 146, 4024-4030 (1991)
MEDLINE 91237115
COMMENT NCBI gi: 193742
FEATURES
source 1..440
/organism="Mus musculus"
/cell_line="hybridoma"
/sequenced_mol="cDNA to mRNA"
39..440
/partial
/note="NCBI gi: 193743"
/codon_start=1
/product="Ab 262.9 heavy chain variable and joining
region"
/translation="MELDLSIPVRNCRCLSEVQLQSGPELVKPGASVKMSCKASGY
TFTDYMKWKQSPGKSLIEWIDPNNGGTSINQKFKGATLVDKSSSTAYMQINS
LTSEDSAVYICARDRYWYFDVWGCTVTWSS"

BASE COUNT 114 a 114 c 110 g 102 t
ORIGIN

Query Match 70.4%; Score 285; DB 55; Length 440;
Best Local Similarity 91.4%; Pred. No. 5.23e-247;
Matches 320; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

Db 34 atgggtgagcctggatcttctctctctctctctcaggaactgcaggtgtct-ctctgag 92
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Qy 1 ATGGGATGCGCGGGGATCTTTCTCTCTCTCTCTGTCAGGAACCTGCAGCTCTCCACTCTGAG 60

Db 93 gtcaactgcacaactctggacctgagctggttaagcctggggcttcagtgaagatgcc 152
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Qy 61 ATCCAGCTCGACGAGCTCGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120

Db 153 tctaaggtcttgatcacacattcactgactacatgaagtgggtgaagcagagccct 212
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 TCGAAGGCTTCTGGTTACTCTATTCACTAGCTATTACATACACTGGGTGAGCAGGCCAT 180

Db 213 ggaagagccttgagtgagtgagattactcctaacaatggtggtactagctacaac 272
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 GGAAGAGCCTTGAGTGGATTGATATATGATCTCTTCAATGCTGTACTAGTACAC 240

Db 273 caaagtccaagggccaagccacattgactgtacaacaatcctccagcacagcctacatg 332
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```









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15

BASE COUNT 91 a 82 c 94 g 80 t 1 others  
ORIGIN  
Query Match 68.6%; Score 278; DB 53; Length 348;  
Best Local Similarity 89.9%; Pred. No. 5.39e-240;  
Matches 312; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Db 2 aggtccagctgcagcagctgacgtgagctggtgaagcctggngcttcagtgaaagtat 61  
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Qy 59 AGATTCAGCTGCAGCAGCTGACCTGACCTGACCTGATGAAGCCTGGGGCTTCAGTGAAGATAT 118  
|||  
Db 62 cctcgaagcttctggtacacatttcactgactacaacatggaactgggtgaagcagagacc 121  
|||  
Qy 119 CCTGAAGGCTTCTGGTACTCATCTAGCTATTACATACACTGGGTGAAGCAGAGCC 178  
|||  
Db 122 atgaaagagccttgagtgattgatattatctcctaacaatgggtgactggctaca 181  
|||  
Qy 179 ATGGAAGAGCCTTCAGTGGATTGATATATTCATCCTTTCAATGGTGGTACTAGCTACA 238  
|||  
Db 182 accaagaagtcaagaagcagccacattgactgtagacaagtcctccagcagacgtaca 241  
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Qy 239 ACCAGAAATTCAGGGCAAGGCCACATTGACTGTTGCAAAATCTTCAGCAGACGCTACA 298  
|||  
Db 242 tggagctccacagcctgacatctgagactctgcaactctattactgtgcaagggaggt 301  
|||  
Qy 299 TGCATCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGGGGGCTA 358  
|||  
Db 302 atacgttcttactggggcgaaggactctggtcactgtctctga 348  
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Qy 359 ACCGCTTTCCTACTGGGGCCAGGGACTCTGGTCACTGTCTGTCCA 405  
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RESULT 13  
LOCUS MUSIGHZF 2908 bp DNA ROD 25-JUL-1991  
DEFINITION Mouse Ig rearranged heavy chain gene V205.12-D-J region, hybridoma A20/44.  
ACCESSION M58535  
KEYWORDS V-region; immunoglobulin heavy chain.  
SOURCE Mouse DNA.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 2908)  
AUTHORS Both, G.W., Taylor, L., Pollard, J.W. and Steele, E.J.  
TITLE Distribution of mutations around rearranged heavy-chain antibody variable-region genes  
JOURNAL Mol. Cell. Biol. 10, 5187-5196 (1990)  
MEDLINE 90377208  
COMMENT NCBI gi: 196346  
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/organism="Mus musculus"  
/strain="C57BL/6J"  
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/sequenced\_mol="DNA"

BASE COUNT 825 a 555 c 676 g 850 t 2 others  
ORIGIN  
Query Match 68.6%; Score 278; DB 56; Length 2908;  
Best Local Similarity 90.1%; Pred. No. 5.39e-240;  
Matches 329; Conservative 0; Mismatches 33; Indels 3; Gaps 2;  
Db 756 caggtgtcctctctgaggtccagctgcaacaatctggacctgaacgggtgaagcctgggg 815

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16

Qy 44 CAGGTGCTCACTCTGAGATCCAGCTGCAGCAGTCTGGACCTGAGCTGAAGCCTGGGG 103  
|||  
Db 816 cttcagtgaaagattctctgaagcttctggatacacagcttcactgactactacaatgaact 875  
|||  
Qy 104 CTTCACTGAGATATCTCTGCAAGGCTTCTGTTACTTACTTACTTACTTACTTACTTACT 163  
|||  
Db 876 ggtgaaacagagccatgaaagagccttgagtgagtgagtgagtgagtgagtgagtgagtg 935  
|||  
Qy 164 GGGTGAAGCAGACCATGAAAGAGCCTTGAGTGGATTGGATATATTGATCTTTCAATG 223  
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Db 936 gtggtactactacaaccagaagttcgaggggcaaggccacattgactgtagacaagtcct 995  
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Qy 224 GTGCTACTAGCTACACCAAAATTCAGGGCAAGGCCACATTGACTGTTGACAAATCTT 283  
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Db 996 ccagcagccctacatgagctccgcagctgacatctgaggagctctgcagctcttact 1055  
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Qy 284 CCAGCAGACCTCATGCTCAGCAGCCTGACATCTGAGGACTCTGAGCTCTTACTTACT 343  
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Db 1056 gtgcaagaggggattacactggttcttactggggcgaaggactctggtcactgtct 1115  
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Qy 344 GTGCAAGGGGGGG--TA-ACCGCTTTGCTTACTGGGGCCAGGGACTCTGGTCACTGTCT 400  
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Db 1116 ctgca 1120  
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Qy 401 CTGCA 405  
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RESULT 14  
LOCUS MUSIGHFX 412 bp mRNA ROD 15-MAR-1990  
DEFINITION Mouse Ig family J558 active mu-chain V-J3 region anti-dextran mRNA, hybridoma 9.14.7.  
ACCESSION M17724  
KEYWORDS C-region; J-region; V-region; immunoglobulin heavy chain; immunoglobulin mu-chain; processed gene.  
SOURCE Mouse (BALB/c) hybridoma cell line 9.14.7., cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 412)  
AUTHORS Akolkar, P.N., Sikder, S.K., Bhattacharya, S.B., Liao, J., Gruero, F., Morrison, S.L. and Kabat, E.A.  
TITLE Different V-L and V-H germ-line genes are used to produce similar combining sites with specificity for alpha-(1->6) dextrans  
JOURNAL J. Immunol. 138, 4472-4479 (1987)  
MEDLINE 87224123  
REFERENCE 2 (bases 1 to 56)  
AUTHORS Akolkar, P.N., Sikder, S.K., Bhattacharya, S.B., Liao, J., Gruero, F., Morrison, S.L. and Kabat, E.A.  
TITLE Errata: Different V-L and V-H germ-line genes are used to produce similar combining sites with specificity for alpha-(1->6) dextrans  
JOURNAL J. Immunol. 139, 3911-3911 (1987)  
COMMENT [2] revises [1].

FEATURES  
source NCBI gi: 195313  
Location/Qualifiers  
1..412  
/organism="Mus musculus"  
sig\_peptide <1..55  
/note="Ig mu heavy chain V-J3-region signal peptide"  
/codon\_start=2  
CDS <1..5412  
/note="Ig mu heavy chain V-J3-region; NCBI gi: 195314"  
/codon\_start=2

/translations="MSWIFLFXLLSCTAGVLSEVQLQSGPELVKPGASVKISKASG  
YTFDTYIMKWKSHGKSLEIGDINPNNGTSTNOKFKGKALFLVDKSSSTAYMOLN  
SLTSEDSAVYYCARDYGSFSFYWGQGLTVTSV"

mat\_peptide 56..>412

/note="Ig mu heavy chain V-J3-region"

/codon\_start=1

BASE COUNT 105 a 94 c 105 g 105 t 3 others

ORIGIN Chromosome 12.

Query Match 67.4%; Score 273; DB 56; Length 412;  
Best Local Similarity 91.1%; Pred. No. 5.47e-235;  
Matches 317; Conservative 0; Mismatches 28; Indels 3; Gaps 2;

Db 1 atggagctgagatctttctcttcmnnctctgtcaggaactcgaggtctcctctcgaggt 60  
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Qy 6 ATGGAGCGGGATCTTCTCTTCCT--TCT-GTCAAGAACTGCAGGCTGCACCTCTGAGAT 62  
Db 61 ccagctgcacaactctggacctgagctggtgaagcctggggcctcagtggaatatcctg 120  
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Qy 63 CCAGCTGCAGCAGTCTGGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCCTG 122  
Db 121 taaggtcttgatcacacattcactgactactacatgaagtgggtgaagcagagtcattg 180  
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Qy 123 CAAAGCTCTGTGTTACTCATTCTACCTAGCTATTACATACACTGGGTGAAGCAGCCATGG 182  
Db 181 aaagagccttgagtggtgagatattaatcctaacaatggtgactagtcacaacca 240  
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Qy 183 AAGAGCCTTGAGTGGATTGGATATATTGATCTTCAATGGTGGTACTAGCTACACCA 242  
Db 241 gaadtcaaggccaagccacatigactgtagacaatcctccagcacagcctacatgca 300  
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Qy 243 GAAATTCAGGGCAAGGCCACATGACTGTGACAAATCTTCCAGCAGCCTACATGCA 302  
Db 301 gctcaacagcctgacatctgaggactctgcagtctattactgtcaag 348  
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Qy 303 TCTCAGCAGCCTGCATCTGAGACTCTGCAGCTCTGAGCTATTACTGTGCAAG 350

RESULT 15  
LOCUS I05341 414 bp DNA PAT 14-NOV-1994  
DEFINITION Sequence 3 from patent EP 0256654.  
ACCESSION I05341  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Schoemaker,H.J. and Sun,L.K.  
TITLE Chimeric rodent/human immunoglobulin specific for tumour-associated antigens  
JOURNAL Patent: EP 0256654-A2 3 24-FEB-1988;

COMMENT NCBI gi: 591098  
FEATURES Location/Qualifiers  
source 1..414  
/organism="unknown"  
BASE COUNT 96 a 97 c 115 g 106 t  
ORIGIN

Query Match 67.4%; Score 273; DB 35; Length 414;  
Best Local Similarity 83.7%; Pred. No. 5.47e-235;  
Matches 339; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Db 10 atggaatggagcagagctttcttctctctctctctctcagtaactgcaggtgttcaatccag 69

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Qy 1 ATGGGATGGAGCGGGATCTTCTCTTCCTCTGTCAAGAACTGCAGGTGTCCACTCTGAG 60  
Db 70 gtccagttgcagcagctctggagctgagctggtgaagcctgggacttcagtgaaagtgctcc 129  
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Qy 61 ATCCAGCTGCAGCAGTCTGGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120  
Db 130 tgaaggtctctggatagacgcttcactaattacttgatagagtggtggttaaacagagagcct 189  
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Qy 121 TGCAGGGCTTCTGGTTACTCATTACTAGCTATTACATACACTGGGTGAAGCAGGCCAT 180  
Db 190 ggacagggccttgagtggaattggggtgatataatcctgggaagtggtggtactaaactacaat 249  
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Qy 181 GAAAGAGCCTTCAGTGGATTGGATATATTGATCTTCAATGGTGTACTAGCTACAAC 240  
Db 250 gagaagttcaaggccaagcaacaactgactgcagacaatactccagcaactgacctacatg 309  
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Qy 241 CAGAAATTCAGGGCCAGGCCACATTGACTGTTCACAAATCTTCCAGCAGCAGCCTACATG 300  
Db 310 cagctcagcagcctgacatctgatgactctgcggtctctattctgtgcaagagatggtccc 369  
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Qy 301 CATCTCAGCAGCCTGCATCTGAGGACTCTGCAGTCTATTACTGTCAAGGGGGGTAAC 360  
Db 370 tggttggttactggggccaaggagcctctggtcaactgtctctgca 414  
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Qy 361 CGCTTTGCTTACTGGGGCCAAGGACTCTGGTCACTGTCTCTGCA 405

Search completed: Mon Jul 8 08:43:12 1996  
Job time : 286 secs.

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mpsrch nn n.a. - n.a. database search. using Smith-Waterman algorithm

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Run on: Mon Jul 8 08:43:30 1996; MasPar time 35.45 Seconds
759.603 Million cell updates/sec
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Tabular output not generated.

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Title:
Description:
>US-08-137-117B-26
(1-405) from US08137117B.seq

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Perfect score: 405  
N.A. Sequence: 1 ATGGGATGGAGCGGATCTT.....CTCTGGTCACTGCTCTGCA 405  
Comp: TACCCCTACCTGCGCCCTAGAA.....GAGACCATGTACACAGACGT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 84802 seqs. 33246950 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-genes22

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16

Statistics: Mean 8.356: Variance 5.470: scale 1.528

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	403	99.5	405	5	Q30754	p12-h2.	1.82e-238
2	301	74.3	443	11	Q45428	KM-750 heavy chain.	2.77e-172
3	293	72.3	449	11	Q45426	KM-796 heavy chain.	4.11e-167
4	280	69.1	474	2	Q12098	Sequence encoding hea	1.02e-158
5	280	69.1	474	2	Q12014	Sequence encoding mou	1.02e-158
6	279	68.9	450	1	Q04695	Heavy chain variable	4.49e-158
7	269	66.4	420	11	Q68700	DRG-200 Ab heavy cha	1.26e-151
8	268	66.2	471	5	Q89607	Co-1 Heavy Chain V Re	5.56e-151
9	267	65.9	499	2	Q11291	Encodes murine monoc	2.45e-150

Reconstituted human antibody to human interleukin-6 receptor -

## ALLEGMENTS

RESULT	1
ID	Q30754 standard; cDNA; 405 BP.
AC	Q30754;
DT	30-MAR-1993 (first entry)
DE	p12-h2.
DD	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
SKW	heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;
KW	plasmid; p12-k2; p12-h2; ss.

Location/Qualifiers

FT	sig peptide	1..57
FT	sig peptide	1..57

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FT /*tag= a
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mat peptide 58..405

FT /\*tag= b

PN W09219759--A.

12-NOV-1992.

24-APR-1992: J00544.

PR—25-APR-1991; JP-095476.

PR 19-FEB-1992; JP-032084.

PA (CHUS ) CHUGAI SEIYAKU KK.

PI Bendig MM. Jones ST. Saldanha JW. Sato K. Tsuchiya M:

DR WPI: 92-398882/48.

DR P-PSDB: R28669.

Reconstituted human

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US-08-137-117B-26.mg

3

PT has low antigenicity and contains mouse V-region complementarity  
PT determining regions  
PS Disclosure; Page 119-120; 207pp; Japanese.  
CC The sequences given in Q30753-54 were used in example to illustrate  
CC the production of a human antibody which recognises human  
CC interleukin-6 receptor (IL-6R). The antibody comprises light (L)  
CC chain and heavy (H) chain variable regions which were derived from a  
CC mouse monoclonal antibody produced from the hybridoma AUK12-20 which  
CC contained the plasmids p12-k2 and p12-k2.  
SQ Sequence 405 BP; 97 A; 97 C; 106 G; 105 T;

Query Match 99.5%; Score 403; DB 5; Length 405;  
Best Local Similarity 99.8%; Pred. No. 1.82e-238;  
Matches 404; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 atgggatggagcgggattcttctcttctgtcaggaaactgcaggtgtccactctgag 60  
Qy 1 ATGGGATGGAGCGGGATCTTCTCTCTCTGTGTCAGGAACCTGCAGGTGTCCACTCTGAG 60  
Db 61 atccagctgcagcagctgcagctcagctcagctgagcctggggttcagtgagatatcc 120  
Qy 61 ATCCAGCTGCAGCAGCTTGGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120  
Db 121 tgcagcgtctgttactcattcactagctattacatacactgggtgaagcagagccat 180  
Qy 121 TCGAAGGCTTCTGGTTACTTATTCCTACTAGTATTACATACACTGGGTGAAGAGCCAT 180  
Db 181 ggaagagcgtgagtgattggatattgatcttcttcatttcatttcagtggtactagctacaac 240  
Qy 181 GGAAAGAGCGCTGACTGGATTGGATATTGATCTCTTCAATGGTGGTACTAGCTACAAC 240  
Db 241 cagaattcaaggcgaaggccacattgactgttgacaaatcttcagcacagcctacatg 300  
Qy 241 CAGAAATTCAGGGCAGGGCCACATTGACTGTGACAAATCTCCAGCAGAGCCTACATG 300  
Db 301 catctcagcagcctgacatctgagcactctgcagctcattactgtgcaaggggggtaac 360  
Qy 301 CATCTCAGCAGCCTGACATCTGAGACTCTGCAGCTATTACTGTGCAGGGGGGTAAAC 360  
Db 361 cctgttctacttggcgaaggcactctggtcactgtctctgca 405  
Qy 361 CGCTTCTCTACTTGGGCCAAGGCACTCTGGTCACTGTCTGTGCA 405

RESULT 2

ID Q45428 standard; cDNA; 443 BP.  
AC Q45428;  
DE 17-NOV-1994 (first entry)  
DT KM-750 heavy chain.  
KW Monoclonal antibody; Ab; ganglioside GM2; chimera;  
KW chimeric antibody; expression vector; heavy; light; chain;  
KW hypervariable region; CDR; constant region; hybridoma;  
KW Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer; ss.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT CDS 33..443  
FT /tag= a  
FT /note= "excluding stop codon"  
FT sig\_peptide 33..89  
FT /tag= b  
FT /note= "sig\_peptide"  
FT misc\_feature 180..194  
FT /tag= c  
FT /note= "hypervariable region 1"

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4

FT misc\_feature 252..287  
FT /tag= d  
FT /note= "hypervariable region 2"  
FT misc\_feature 384..410  
FT /tag= e  
FT /note= "hypervariable region 3"  
PN AU9346181-A.  
PD 17-MAR-1994. 046181.  
PF 07-SEP-1993; 046181.  
PR 07-SEP-1992; JP-238452.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;  
PI Shitara K;  
DR WPI; 94-126857/16.  
DR P-PSDB; R53330.  
PT Humanised antibody specific for ganglioside GM2 - used for  
PT producing a cytotoxic effect on cancers such as melanoma,  
PT neuroblastoma and glioma.  
PS Disclosure; Page 107-108; 191pp; English.  
CC Chimeric human Ab expression vectors are constructed by inserting  
CC the Ab heavy and light chain variable region-encoding cDNA  
CC isolated from hybridomas producing a mouse or rat monoclonal Ab  
CC reacting with the ganglioside GM2 respectively into an expression  
CC vector for use in animal cells which contains the human Ab heavy and  
CC light chain constant region-encoding cDNA. The expression vectors  
CC are introduced into animal cells and the transformant thus obtained  
CC is cultured for the prodn. of a chimeric human Ab reacting with the  
CC ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric  
CC human Abs will not cause anti-mouse Ig Ab prodn. in the patient's  
CC body but show a prolonged blood half-life, with a reduced frequency  
CC of adverse effects, so that it can be expected to be superior  
CC to mouse monoclonal Abs in the efficacy in the treatment of human  
CC cancer, for instance.  
CC Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603  
CC heavy and light chain sequences are given in Q45426-30.  
CC CDR regions for use in chimeric Abs are indicated in the  
CC Features Table.  
SQ Sequence 443 BP; 109 A; 112 C; 119 G; 103 T;

Query Match 74.3%; Score 301; DB 11; Length 443;  
Best Local Similarity 90.3%; Pred. No. 2.77e-172;  
Matches 371; Conservative 0; Mismatches 34; Indels 6; Gaps 4;

Db 33 atgggatggagctggtattcttctctctctgtcaggaaactgcaggtgtcctctctgag 92  
Qy 1 ATGGGATGGAGCGGGATCTTCTCTCTCTCTGTGTCAGGAACCTGCAGGTGTCCACTCTGAG 60  
Db 93 gtccagctgcagcagctctggacctgagctgggtgaagcctggggcttcagtgagatatcc 152  
Qy 61 ATCCAGCTGCAGCAGCTGCGACCTGAGCTGATGAAGCCTCGGGCTTCAGTGAAGATATCC 120  
Db 153 tgcagcgtctctggatcacattcactgactacaacatggactgggtgaagcagagccat 212  
Qy 121 TCGAAGGCTTCTGGTTACTTCACTTACATACATACACTGGGTGAGCAGAGCCAT 180  
Db 213 ggaagagccttgagtggtggatattatttacttaacaatgggtgactggtctacaac 272  
Qy 181 GGAAAGAGCGCTTGGTGGATATGATATGATCTTCAATGGTGGTACTAGCTACAAC 240  
Db 273 cagaagtccaagagcagggcacattgactgtacacagtcctccagcagcctacatg 332  
Qy 241 CAGAAATTCAGGGCAAGGCCACATTCAGCTGTTCACAAATCTCCAGCAGAGCCTACATG 300  
Db 333 gagctccagcgtgcacatctgaggactctgagactctgcagctctattactgtgcaagagcgggag 392

QY 301 CATCTCAGCAGCCTGCATCTCAGGACTTGCAGTCTATTACTGTGCAAG-C-GGGG-GT 357

Db 393 tattactacgcttggactggggcccaaggagactctggtcaactgtctctga 443

QY 358 AACCGCTTTGGCTT---ACTGGGGCAAGGACTGTGTCACTGCTCTTGA 405

RESULT	3	
ID	Q45426	standard; cDNA; 449 BP.
AC	Q45426;	
DT	17-NOV-1994	(first entry)
DE	KM-796	heavy chain.
KE	Monoclonal antibody; Ab;	ganglioside
KW	chimeric antibody; expression vector	
KW	hypervariable region; CDR; constant	
KW	Ig; immunoglobulin; KM-796; KM-750;	
OS	Mus musculus.	
FT	Key	Location/Qualifiers
FE	CD5	33..449

FT	/note= "excluding stop codon"
FT	sig_peptide 33..89
FT	/*tag= b
FT	/note= "sig_peptide"
FT	misc_feature 180..194
FT	/*tag= c
FT	/note= "hypervariable region 1;
FT	claim 8"
FT	misc_feature 237..287
FT	/*tag= d
FT	/note= "hypervariable region 2;
FT	claim 8"
FT	misc_feature 384..416
FT	/*tag= e
FT	/note= "hypervariable region 3;
FT	claim 8"
PN	AU9346181-A.
PD	17-MAR-1994.
PF	07-SEP-1993; 046181.
PR	07-SEP-1992; JP-238452.
PA	(KYOW ) KYOWA HAKKO KOCYO KK.
PI	Hanai N, Hasegawa M, Koike M,
PI	Shitara K;
DR	WPI; 94-126057/16.
	Kuwana Y, Nakamura K;

Humanised antibody specific for ganglioside GM2 - used for producing a cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma. Claim 5; Page 104-105; 191pp; English.

Chimeric human Ab expression vectors are constructed by inserting the Ab heavy and light chain variable region-encoding cDNA isolated from hybridomas producing a mouse or rat monoclonal Ab reacting with the ganglioside GM2 respectively into an expression vector for use in animal cells which contains the human Ab heavy and light chain constant region-encoding cDNA. The expression vectors are introduced into animal cells and the transformant thus obtained is cultured for the prodn. of a chimeric human Ab reacting with the ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric human Abs will not cause anti-mouse Ig Ab prodn. in the patient's body but show a prolonged blood half-life, with a reduced frequency of adverse effects, so that it can be expected to be superior to mouse monoclonal Abs in the efficacy in the treatment of human cancer, for instance.

CC	Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603 heavy and light chain sequences are given in Q45426-30.
CC	CDR regions for use in chimeric Abs are indicated in the Features Table.
CC	Sequence 449 BP; 108 A; 116 C; 113 G; 112 T;
Query Match	72.3%; Score 293; DB 11; Length 449;
Best Local Similarity	92.2%; Pred. No. 4,11e-167;
Matches	320; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Db	33 atgggatggagctggatctttctctctctctgtccagaaactgcaggtgctctctctgag 92
Qy	1 ATCGGATGGACCGGGATCTTCTCTCTCTCTGTCAGCAACTGCGAGGTGCGACTCTGAG 60
Db	93 gtcacgtgcacgagctgtggacctgagctgggtgaagcctggggcttcagtgaagatactc 152
Qy	61 ATCCAGCTGCGACGAGCTGGGACCTGCAGCTCATGAAGCCTGGGGCTTCAGTGAAGATGCC 120
Db	153 tgcgaagctctctggatacacattcaactgactacacacatgaactgggtgaagcagagccat 212
Qy	121 TCGAAGGCTTCTGGTTACTCATTTCACTAGCTATTACATACACTGGGTGCAAGCAGGCCAT 180
Db	213 ggaagagccttgagtgagtggttatattctctacaaatgggtgaactggctacaac 272
Qy	191 GGAAGACGCTTGCTGCTGGATGGGATATATGATCTCTTCAATGGCTGCTACTGCTACAAAC 240
Db	273 cagaagttcaagagcaaggccacattgactgtadagaagctctccagcacagcgtcacatg 332
Qy	241 CAGAAATTCAAAGGCGAAGGCCACATTGACTGTTTGAAGAAATCTTCCAGACAGCGCTACATG 300
Db	333 gagctccacagcctgacatctggaggacctgcagctctattactgtgc 379
Qy	301 CACTCCAGCAGCTGCATCTCGAGCACTGCGACTCTGCGTCTATTACTGTGC 347

RESULT	4
ID	Q12058 standard; DNA; 474 BP.
AC	Q12058;
DT	15-AUG-1991 (first entry)
DE	Sequence encoding heavy chain variable region of murine
DE	2G12 immunoglobulin.
KW	Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.
OS	Mus musculus.
FH	Key
FT	Location/Qualifiers
FT	52..474
FT	/*tag= a
FT	/product= mouse MAb 2G12 H-chain variable region
PN	W09107493-A.
PD	30-MAY-1991.
PF	13-NOV-1990; U06615.
PR	13-NOV-1989; US-433730.
PA	(XOMA-) XOMA CORP.
PA	(GREC ) GREEN CROSS CORP.
PI	Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
DR	WPI; 91-178044/24.
DR	p-PSDR: R12356.

PT New chimeric mouse-human antibodies - used to detect, kill and  
PS remove HIV-1 antigen from sample  
PS Disclosure; fig 7; 107pp; English.  
CC This sequence encodes the heavy chain variable (V) region of a  
CC mouse monoclonal antibody (MAB), 2G12, specific for an HIV-1  
CC viral antigen. It is used in the construction of a chimeric MAB  
CC comprising heavy and light chains having murine V regions and human  
CC C regions. The chimeric MABs are more effective than murine MAB

CC 2G12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAb can be used as immun-conjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV.

CC See also Q12056-57 and Q12059-63.

SQ Sequence 474 BP; 123 A; 118 C; 112 G; 121 T;

Query Match 69.1%; Score 280; DB 2; Length 474;  
Best Local Similarity 88.5%; Pred. No. 1.02e-158;  
Matches 322; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
Db 52 atggatgagctgagctcttcttctctctgcaggaactgcagctgctctctctgag 111  
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Qy 1 ATGGGATGGAGCGGATCTTCTCTCTCTCTGTCAGGAACCTGCAGGCTCTCAG 60  
Db 112 gtcagctgcaacagctctggaactgaactggtgaagctggggttcagtgagatatcc 171  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 61 ATCCAGCTGCAGCAGCTGCAGCTGAGCTGATGAAGCTGGGGCTTCAGTGAAGATATCC 120  
Db 172 tgaagactctggtatcacattcactgaatacaccatacactgggtgaagcagagccat 231  
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Qy 121 TCGAAGCCTTCTGTTACTTACTAGCTATTATACATACACTGGGTGAAGCAGGCGAT 180  
Db 232 ggacagagcttgagtgattggaggatttaatacctaacaatggtggtactacctacaac 291  
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Qy 181 CGAAGAGCCTTGAGTGGATATATGATCTCTTTCATGCTGGTGTACTAGCTACAAC 240  
Db 292 cagaagttcaaggagcagccacattgattgtagaagctcctccagcagcctacatg 351  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 241 CAGAAATCAAGGGCAAGGCCACATTGACTGTTGACAAATCTTCCAGCAGCCTACATG 300  
Db 352 gacgtccgagcctgacatctgattctgagctcagctctattactgtgcaagaagagaaat 411  
| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 301 CATCTCAGCAGCCTGACATCTGAGGACTCTGCGACTCTGCGTCTATTACTGTGCAAGGGGGGTAAC 360  
Db 412 ctct 415  
| ||  
Qy 361 CGCT 364

RESULT 5  
ID Q12014 standard; DNA; 474 BP.  
AC Q12014;  
DT 19-AUG-1991 (first entry)  
DE Sequence encoding mouse MAb 2G12 H chain V region.  
KW HIV-1; chimera; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 52..474  
FT /\*tag= a  
PN W09107494-A.  
PD 30-MAY-1991.  
PF 13-NOV-1990; 006627.  
PR 13-NOV-1989; US-433703.  
RA (XOMA-) Xoma Corp.  
PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;  
DR WPI; 91-178106/24.  
P-PSDB; R12234.  
PT New chimeric mouse human antibodies - used in treatment, diagnosis  
PT and prophylaxis of HIV infections.  
PS Disclosure; Fig 7; 10pp; English.  
CC The mouse VH gene product may be used to produce chimeric mouse-

CC human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in CC treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system.

SQ Sequence 474 BP; 123 A; 118 C; 112 G; 121 T;

Query Match 69.1%; Score 280; DB 2; Length 474;  
Best Local Similarity 88.5%; Pred. No. 1.02e-158;  
Matches 322; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
Db 52 atggatgagctgagctcttcttctctctgcaggaactgcaggtgctctctctgag 111  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 1 ATGGGATGGAGCGGATCTTCTCTCTCTCTGTCAGGAACCTGCAGGCTCTCAG 60  
Db 112 gtcagctgcaacagctctggaactgaactggtgaagctggggttcagtgagatatcc 171  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 61 ATCCAGCTGCAGCAGCTTGCAGCTGAGCTGATGAAGCTGGGGCTTCAGTGAAGATATCC 120  
Db 172 tgaagactctggtatcacattcactgaatacaccatacactgggtgaagcagagccat 231  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 121 TCGAAGCCTTCTGTTACTTACTAGCTATTATACATACACTGGGTGAAGCAGGCGAT 180  
Db 232 ggacagagcttgagtgattggaggatttaatacctaacaatggtggtactacctacaac 291  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 181 CGAAGAGCCTTGAGTGGATATATGATCTCTTTCATGCTGGTGTACTAGCTACAAC 240  
Db 292 cagaagttcaaggagcagccacattgattgtagaagctcctccagcagcctacatg 351  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 241 CAGAAATCAAGGGCAAGGCCACATTGACTGTTGACAAATCTTCCAGCAGCCTACATG 300  
Db 352 gacgtccgagcctgacatctgattctgagctcagctctattactgtgcaagaagagaaat 411  
| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 301 CATCTCAGCAGCCTGACATCTGAGGACTCTGCGACTCTATTACTGTGCAAGGGGGGTAAC 360  
Db 412 ctct 415  
| ||  
Qy 361 CGCT 364

RESULT 6  
ID Q04695 standard; DNA; 450 BP.  
AC Q04695;  
DT 04-OCT-1990 (first entry)  
DE Heavy chain variable domain of human chorion gonadotrophin-binding pptd.  
KW Human chorionic gonadotropin; antibodies; heavy chain; chorioncarcinoma;  
KW abortion; tumour detection; complementary determining regions;  
KW pregnancyprevention; ss.  
OS Mus musculus.  
FH Key Location/Qualifiers  
FT CDS 39..449  
FT /\*tag= a  
FT /product=hCG-binding protein heavy chain variable region  
FT misc feature 187..200  
FT /\*tag= b  
FT /product=CDR  
FT misc feature 247..293  
FT /\*tag= c  
FT /product=CDR  
FT misc feature 390..416  
FT /\*tag= d  
FT /product=CDR  
FT misc feature 1..6  
FT /\*tag= e  
FT /label=EcoRI-linker







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Qy 241 CAGAAATTCAGGCGCAGCCACATTCGACTGTGACAAATCTTCACGACACGCCTACATG 300

Db 341 cacctcaagagcctgacatctgagactctgcagctctgagctattactgtgtaagcgg 393

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 301 CATCTCAGCAGCCTGACATCTCAGGACTCTCGACTCTATTACTCTATTACTGTGCAAGGG 353

RESULT 10

ID Q43385 standard; cDNA to mRNA; 588 BP.

AC Q43385;

DT 26-OCT-1993 (first entry)

DE H-chain V-region of monoclonal antibody A23A41.

KW MAb; I; light; H; heavy; Ig; immunoglobulin; V; variable; C; constant;

KW J; joining; hybridoma; interleukin-2 receptor; IL-2R; gamma1;

KW kappa; PCR; polymerase chain reaction; ss.

OS Mus sp.

FH Key Location/Qualifiers

FT CDS 134..583

FT /\*tag= a

FT mat\_peptide 192..583

FT /\*tag= b

FT sig\_peptide 134..191

FT /\*tag= c

PN EP-547631-A.

PD 23-JUN-1993.

PF 18-DEC-1992; 121630.

PR 19-DEC-1991; DE-142077.

PA (BOE ) BOEHRINGER MANNHEIM GMBH.

PI Betzl G, Kaluza B, Weidle UH;

DR WPI; 93-198643/25.

DR P-PSDB; R37681.

PT Vector for immunoglobulin expression without coding sequence

PT variations - includes variable region DNA fragment contg. part of

PT leader protein to provide high antibody yields in lymphoid cells

PS Example 1; Page 16; 35pp; German.

CC Murine hybridoma A23A41 expresses an antibody against the beta chain

CC of human interleukin-2 receptor. This antibody consists of a heavy

CC chain of isotype gamma1 and a light chain of isotype kappa. Kappa

CC primers (Q43386-87) and gamma1 primers (Q43388-89) are used in the

CC PCR for the isolation of appropriate DNA fragments (Q43384-85).

SQ Sequence 588 BP; 148 A; 165 C; 134 G; 140 T;

Query Match 65.9%; Score 267; DB 7; Length 588;

Best Local Similarity 86.4%; Pred. No. 2.45e-150;

Matches 317; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 134 atggaatgagctggatcttctctctctctctctctctctctctctctctctctctctgag 193

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Qy 1 ATGGGATGGAGCGGGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAG 60

Db 194 gtccagctgcaacagtttgagctgaattgggtgaagcctggagcttcgtggaagatatcc 253

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 61 ATCCAGCTGCAGCAGCTCTGGACCTGAGCTGATGAGGCTGGGGCTTCAGTGAAGATATCC 120

Db 254 tgcaaggctctggctacattttcactgactacaacatggaactgggtggaagcagagccat 313

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 121 TGCAGAGCTTCGTGGTTACTCATCTACTAGCTATTACATCAGCTGGGTGAGAGAGCCAT 180

Db 314 ggaagagccttgagtgattgagatattgatcctcaacttttgatagttccagttacacac 373

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 181 GGAAGAGCCCTTGAGTGGATGGCATATATTCATCTCTTTCAATCGTGGTACTGTACATCAAC 240

Db 374 cagaagtccaaggaagccacattgactgtagacaagtcctccaacacacagcactacatg 433

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Qy 241 CAGAAATTCAGGCGCAGCCACATTCGACTGTGACAAATCTTCACGACACGCCTACATG 300

Db 434 gactccgcagcctgacatctgagacactgcagctctattactgtgcaagaggggattc 493

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 301 CATCTCAGCAGCCTGACATCTGAGGACTCTCGACTCTATTACTGTGCAAGGGGGGTAC 360

Db 494 ccctatg 500

|||||

Qy 361 CGCTTTG 367

RESULT 11

ID Q43843 standard; DNA; 417 BP.

AC Q43843;

DT 20-OCT-1993 (first entry)

DE Chimeric 128.1 VH, mouse gamma subgroup IIB DNA.

KW Polymerase chain reaction; primer; PCR; amplify; murine; heavy;

KW light; chain; variable; constant; region; anti-human; transferrin;

KW receptor; antibody; brain; capillary; endothelial cell; conjugate;

KW neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke;

KW epilepsy; Parkinsons disease; Alzheimers disease; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT sig\_peptide 1..57

FT /\*tag= a

FT /note= "leader sequence"

FT mat\_peptide 58..417

FT /\*tag= b

PN W09310819-A.

PD 10-JUN-1993.

PF 24-NOV-1992; U10206.

PR 26-NOV-1991; US-800458.

PA (ALKE-) ALKERMES INC.

PI Friden PM;

DR WPI; 93-196742/24.

DR P-PSDB; R38259.

PT Antibody conjugates specific for transferrin receptor - used for

PT diagnosis and treatment of cancer, AIDS and neurological

PT disorders

PS Table 6; Page 57; 151pp; English.

CC The sequences given in Q43842-43 encode the light and heavy chains,

CC respectively, of the chimeric antibody 128.1. 128.1 is an anti-human

CC transferrin receptor antibody which binds to the transferrin receptor

CC on brain capillary endothelial cells. This antibody may be used in a

CC conjugate in which it is linked to a neuropharmaceutical or diagnostic

CC agent. The conjugate may be used to treat or prevent neurological

CC disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and

CC Alzheimers disease. It may also be used for diagnostic methods.

SQ Sequence 417 BP; 102 A; 104 C; 102 G; 103 T;

Query Match 64.9%; Score 263; DB 7; Length 417;

Best Local Similarity 87.3%; Pred. No. 9.25e-148;

Matches 308; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 1 atggaatgagctgggtaatgctctctctctctctctctctctctctctctctctctctgag 60

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Qy 1 ATGGGATGGAGCGGGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAG 60

Db 61 gtccagctgcaacagctctggacctgaactgggtgaagcctggagcttcaatgaagattccc 120

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Qy 61 ATCCAGCTGCAGCAGCTCTCGAGCTGAGGCTGGGGCTTCAGTGAAGATATCC 120

Db 121 tqcaaggctcttggttaactcattcactggctacaccatgaactgggtgaagcagagccat 180

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17

```
FT CDS 4999..5034
FT /*tag= c
FT /note= "Undefined ORF1"
FT CDS 5153..5482
FT /*tag= d
FT /note= "Undefined ORF2"
FT CDS 5580..5900
FT /*tag= e
FT /note= "Undefined ORF3"
FT unsure 6128..6329
FT /*tag= f
FT unsure 6336..6635
FT /*tag= g
PN W09310819-A.
PD 10-JUN-1993.
PF 24-NOV-1992; U10206.
PR 26-NOV-1991; US-800458.
PA (ALKE-) ALKERMES INC.
PI Friden PM;
DR P-PSDB; R41715-18.
PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders
PS Disclosure; Fig 19A-F; 151pp; English.
CC The sequences given in Q43846-48 represent the expression vectors
CC pAH4625, pAH4807 and pAH4808. These vectors represent the cloning
CC of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4
CC respectively, with the variable region of the murine monoclonal
CC antibody 128.1. These plasmids each encode a chimeric monoclonal
CC antibody in which the heavy chain (VH) is derived from a murine
CC source and the sequences encoding CH1, CH2 and CH3 are derived from
CC a human source. These vectors in combination with the chimeric light
CC chain vector, pAG4611 (see also Q43845), were transfected into SP2/0
CC cells and clones were isolated. Antibody analysis using biosynthe-
CC tically labelled proteins, immunoprecipitation and SDS-PAGE indicated
CC appropriate bands for the heavy and light chains as well as the
CC assembled antibody for the gamma-3 and gamma-4 chimeras. No detectable
CC protein was isolated for the gamma-2 transfectants. 128.1 is an anti-
CC human transferrin receptor antibody which binds to the transferrin
CC receptor on brain capillary endothelial cells. This antibody may be
CC used in a conjugate in which it is linked to a neuropharmaceutical or
CC diagnostic agent. The conjugate may be used to treat or prevent
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC methods.
SQ Sequence 10844 BP; 2173 A; 2228 C; 2150 G; 2063 T;

Query Match 64.9%; Score 263; DB 7; Length 10844;
Best Local Similarity 87.3%; Pred. No. 9.25e-148;
Matches 308; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 3907 atggaatggagctgggaatgctctctctcctgtcaggaaactgcaggtgtccgctctgag 3966
||||| ||||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 ATGGGATGGAGCGGGGATCTTCTCTCTCTGTCTGTCAGGAACATGCAGGTTGTCACACTCTGAG 60

Db 3967 gtccagctcaacagtctggacctgaactgggtgaagcctggagcttcaatgaagattcc 4026
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 ATCCAGCTGCAGCAGTCTGGACCTGAGCTGATGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120

Db 4027 tqcaaggtcttctgttactcattcaactgaacctacaccatgaactgggtgaagcagagccat 4086
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 TCGAAGGCTTCGTGTTACTTACTTACTAGTATTACATACACTGCTGGTGAAGCAGGCGCAT 180
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Db 4087 ggagagaacctgagtgattggaactattaactcctcacaatgggtggtactgactacaac 4146
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 GGAAGAGCCCTTGAGTGGATTGGATATATTGATCTTTCAATGCTGTGTACTAGTACAAC 240

Db 4147 cagaagtcgaagacaagggcccttttaactctagacaagctatccacaacagccctacatg 4206
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 CAGAAATTCGAAGGGCAAGGCCACATTGACTCTTGACAAATCTTCAGCAGCAGCCATACG 300

Db 4207 gagctcctcagctctgacatctgagagcctctgcagctctattactgtgcaagagg 4259
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 CATCTCAGCAGCCTGACATCTGAGGACTCTCGACTCTATTACTCTGCAAGGGG 353

RESULT 14
ID Q43844 standard; DNA; 11529 BP.
AC Q43844;
DT 20-OCT-1993 (first entry)
DE Plasmid pAH4602.
KW Polymerase chain reaction; primer; PCR; amplify; murine;
KW heavy/light; chain; variable; constant; region; anti-human;
KW transferrin; receptor; antibody; brain; capillary;
KW endothelial cell; conjugate; neuropharmaceutical;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy;
KW Parkinsons disease; Alzheimers disease; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT unsure 2070..3769
FT /*tag= a 3907..4611
FT CDS
FT /*tag= b
FT /note= "VH and CH DNA derived by PCR"
FT sig_peptide 3097..3963
FT /*tag= c
FT /note= "Leader sequence"
FT mat_peptide 3964..4611
FT /*tag= d
FT /note= "Mature VH/CH region"
FT CDS 5000..5044
FT /*tag= e
FT /note= "Undefined ORF"
FT CDS 5163..5492
FT /*tag= f
FT /note= "Undefined ORF2"
FT CDS 5589..5909
FT /*tag= g
FT /note= "Undefined ORF2"
FT unsure 6118..7321
FT /*tag= h 8177..8201
FT unsure
FT /*tag= i
PN W09310819-A.
PD 10-JUN-1993.
PF 24-NOV-1992; U10206.
PR 26-NOV-1991; US-800458.
PA (ALKE-) ALKERMES INC.
PI Friden PM;
DR WPI; 93-196742/24.
DR P-PSDB; R41682-85.
PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders
PS Disclosure; Fig 11A-G; 151pp; English.
CC This sequence represents the expression vector pAH4602.
CC This vector contains open reading frames encoding the heavy
```

CC chain variable region (VH) of the antibody 128.1, an  
CC ampicillin resistance gene and a histidine (histidinol)  
CC selection marker. Transcription of the VH gene is from the  
CC VH promoter of the murine 27.44 gene. The vector also  
CC includes a heavy chain immunoglobulin enhancer and the human  
CC gamma1 constant region (CH). The VH region of 128.1 was  
CC isolated by polymerase chain reaction and cloned into  
CC plasmid pAH4274. This was achieved by digesting the plasmid  
CC and the product with EcoRV and NheI. The VH gene was  
CC inserted in-frame with the human gamma1 CH region. 128.1 is  
CC 3' end of the VH-J region by means of a NheI site. 128.1 is  
CC an anti-human transferrin receptor antibody which binds to  
CC the transferrin receptor on brain capillary endothelial  
CC cells. This antibody may be used in a conjugate in which it  
CC is linked to a neuropharmaceutical or diagnostic agent. The  
CC conjugate may be used to treat or prevent neurological  
CC disorders eg. brain tumours, AIDS, stroke, epilepsy,  
CC Parkinsons and Alzheimers disease. It may also be used for  
CC diagnostic methods.  
SQ Sequence 11529 BP; 2175 A; 2217 C; 2148 G; 2058 T;

Query Match 64.9%; Score 263; DB 7; Length 11529;  
Best Local Similarity 87.3%; Pred. No. 9,25e-148;  
Matches 308; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 3907 atggaatgagctgggtgaatgctctcctgtcaggaactgaggtgcgcgtctgag 3966  
Qy 1 ATGGGATGAGGGGATCTTTCTCTCTCTGTCAGAACTGCAGGCTGCCACTCTGAG 60  
Db 3967 gtccagctcaacagtctgagccctgaactgggtgaagccttcaatgaagattcc 4026  
Qy 61 ATCCAGCTGCAGAGCTGCGACCTGAGCTGAGCTGGGGCTTCAGTGAAGATATCC 120  
Db 4027 tgcaggtcttgtaactcattcactgctacacatgaactgggtgaagcagagccat 4086  
Qy 121 TCGAAGGCTTCTGTTACTTCACTTCACTAGTATTACATACACTGGGTGAAGCAGCCAT 180  
Db 4087 ggagagaacctgagtgagtgagctattaatcctcacaatgggtgtaactgactacaac 4146  
Qy 181 GGAAGAGGCTTGAGTGCATTGATATATTGATCCTTCAATGGTGGTACTAGTACAAC 240  
Db 4147 cagaagttcaagacaaggcccttaactgtgacaagtcacacacagcctacatg 4206  
Qy 241 CAGAAATTCAGGGCAGGCCACATTGACTGTTGACAAATCTTCACGACAGCCATACG 300  
Db 4207 gagctcctcagctgacatctgaggaactctgagcttactattactgtgaagagg 4259  
Qy 301 CATCTCAGCAGGCTGACATCTGAGCACTGCGAGCTCTGAGTCTATTACTGTGCAAGGG 353

## RESULT 15

ID Q43847 standard; DNA; 12132 BP.  
AC Q43847;  
DT 20-OCT-1993 (first entry)  
DE Plasmid pAH4807.  
KW Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625;  
KW heavy; light; chain; variable; constant; region; anti-human; pAH4807;  
KW transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2;  
KW endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4;  
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal;  
KW Parkinsons disease; Alzheimers disease; SP2/0 cell; ss.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT unsure 11..11710

FT /\*tag= a 1848..2546  
FT CDS /\*tag= b  
FT /\*note= \*128.1 VH/human gamma-3 CH1\*  
FT CDS 2939..2980  
FT /\*tag= c  
FT /\*note= "Undefined ORF1"  
FT CDS 3133..3177  
FT /\*tag= d  
FT /\*note= "Undefined ORF2"  
FT CDS 3672..4001  
FT /\*tag= e  
FT /\*note= "Undefined ORF3"  
FT CDS 4099..4419  
FT /\*tag= f  
FT /\*note= "Undefined ORF4"  
FT unsure 4630..5559  
FT /\*tag= g  
FT unsure 5566..5864  
FT /\*tag= h  
FT unsure 6720..6744  
FT /\*tag= i  
FN W09310819-A.  
PD 10-JUN-1993.  
PF 24-NOV-1992; U10206.  
PR 26-NOV-1991; US-800458.  
PA (ALKE-) ALKERMES INC.  
PI Friden PW;  
DR WPI; 93-196742/24.  
DR P-PSDB; R41710-14.  
PT Antibody conjugates specific for transferrin receptor - used  
PT for diagnosis and treatment of cancer, AIDS and neurological  
PT disorders  
PS Disclosure; Fig 18A-F; 151pp; English.  
CC The sequences given in Q43846-48 represent the expression vectors  
CC pAH4625, pAH4807 and pAH4808. These vectors represent the cloning  
CC of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4  
CC respectively, with the variable region of the murine monoclonal  
CC antibody 128.1. These plasmids each encode a chimeric monoclonal  
CC antibody in which the heavy chain (VH) is derived from a murine  
CC source and the sequences encoding CH1, CH2 and CH3 are derived from  
CC a human source. These vectors in combination with the chimeric light  
CC chain vector, pAH4611 (see also Q43845), were transfected into SP2/0  
CC cells and clones were isolated. Antibody analysis using biosynthe-  
CC tically labelled proteins, immunoprecipitation and SDS-PAGE indicated  
CC appropriate bands for the heavy and light chains as well as the  
CC assembled antibody for the gamma-3 and gamma-4 chimeras. No detectable  
CC protein was isolated for the gamma-2 transfectants. 128.1 is an anti-  
CC human transferrin receptor antibody which binds to the transferrin  
CC receptor on brain capillary endothelial cells. This antibody may be  
CC used in a conjugate in which it is linked to a neuropharmaceutical or  
CC diagnostic agent. The conjugate may be used to treat or prevent  
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,  
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic  
CC methods.  
SQ Sequence 12132 BP; 2292 A; 2441 C; 2285 G; 2156 T;

Query Match 64.9%; Score 263; DB 7; Length 12132;  
Best Local Similarity 87.3%; Pred. No. 9,25e-148;  
Matches 308; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 1848 atggaatgagctgggtgaatgctctcctgtcaggaactgaggtgcgcgtctgag 1907  
Qy 1 ATGGGATGAGGGGATCTTTCTCTCTCTGTCAGAACTGCAGGCTGCCACTCTGAG 60



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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:44:30 1996; MasPar time 187.70 Seconds

Tabular output not generated. 775.696 Million cell updates/sec

Title: >US-08-137-117B-26

Description: (1-405) from US08137117B.seq

Perfect Score: 405

N.A. Sequence: 1 ATGGGATGGAGCGGATCTT.....CTCTGTCACGTCTCTGCA 405

Comp: TACCTACTCGCCCTAGAA.....GAGCAGTGACAGACGT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-STs

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56  
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62  
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80  
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86  
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92  
93:EST93 94:EST94  
95:EST95 96:EST96 97:EST97 98:EST98 99:EST99  
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109  
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114  
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119  
120:EST120 121:EST121 122:EST122 123:EST123  
124:EST124 125:EST125 126:EST126 127:EST127

Database: EST-STs-TWO

95:EST95 96:EST96 97:EST97 98:EST98 99:EST99  
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109  
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114  
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119  
120:EST120 121:EST121 122:EST122 123:EST123  
124:EST124 125:EST125 126:EST126 127:EST127

128:enEST20 129:enEST1 130:enSTS1 131:enSTS2 132:enSTS3

Statistics: Mean 10.062; Variance 1.818; scale 5.534

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
	1	100	24.7	287	69	T27609	EST101034	Homo sapien	1.46e-157
	2	100	24.7	287	127	HS272609	EST101034	Homo sapien	1.46e-157
	3	95	23.5	238	122	HS67011	EST89669	Homo sapiens	9.24e-147
	4	95	23.5	238	70	T29670	EST89669	Homo sapiens	9.24e-147
c	5	88	21.7	209	125	HS93811	EST61186	Homo sapiens	9.47e-132
c	6	88	21.7	209	70	T28938	EST61186	Homo sapiens	9.47e-132
	7	72	17.8	385	58	R86288	yp12e09.r1	Homo sapie	4.76e-98
	8	54	13.3	299	69	T27727	EST13874	Homo sapiens	1.35e-61
	9	54	13.3	299	127	HS272727	EST13874	Homo sapiens	1.35e-61
	10	51	12.6	330	64	SSCID10	S.scrofa mRNA; expres	9.76e-56	56
	11	51	12.6	330	129	SSCID10	S.scrofa mRNA; expres	9.76e-56	56
	12	43	10.6	169	79	T64512	yc24f06.r1	Homo sapie	1.53e-40
	13	43	10.6	303	57	R83139	yp1lg03.r1	Homo sapie	1.53e-40
	14	43	10.6	419	100	H73816	ye11b01.r1	Homo sapie	1.53e-40
	15	43	10.6	419	124	HS816226	ye11b01.r1	Homo sapie	1.53e-40
	16	42	10.4	297	127	HS27868	EST18962	Homo sapiens	1.08e-38
	17	42	10.4	297	69	T27868	EST18962	Homo sapiens	1.08e-38
	18	39	9.6	430	123	HS787240	yj91h09.r1	Homo sapie	3.11e-33
	19	39	9.6	430	54	R72787	yj91h09.r1	Homo sapie	3.11e-33
	20	35	8.6	478	123	HS753236	yp21g01.r1	Homo sapie	3.58e-26
	21	35	8.6	478	16	H43753	yp21g01.r1	Homo sapie	3.58e-26
	22	29	7.2	97	17	H44771	yp20e11.r1	Homo sapie	3.50e-16
	23	29	7.2	97	123	HS771238	yp20e11.r1	Homo sapie	3.50e-16
	24	29	7.2	147	16	H42647	yp13a12.r1	Homo sapie	3.50e-16
	25	29	7.2	331	127	HS277115	EST13381	Homo sapiens	3.50e-16
	26	29	7.2	331	69	T27715	EST13381	Homo sapiens	3.50e-16
	27	28	6.9	228	11	H24604	y140b06.r1	Homo sapie	1.32e-14
	28	27	6.7	169	47	R48619	yj68a01.r1	Homo sapie	4.68e-13
	29	27	6.7	174	70	T29212	EST73046	Homo sapiens	4.68e-13
	30	27	6.7	174	116	HS21211	EST73046	Homo sapiens	4.68e-13
	31	27	6.7	234	127	HS278164	EST30734	Homo sapiens	4.68e-13
	32	27	6.7	234	69	T28164	EST30734	Homo sapiens	4.68e-13
	33	27	6.7	325	122	HS71611	EST91759	Homo sapiens	4.68e-13
	34	27	6.7	325	70	T29716	EST91759	Homo sapiens	4.68e-13
	35	26	6.4	367	78	T60021	yc01g07.r1	Homo sapie	1.54e-11
	36	26	6.4	369	10	H22104	y134f04.r1	Homo sapie	1.54e-11
	37	25	6.2	253	70	T29661	EST89449	Homo sapiens	4.67e-10
	38	25	6.2	253	122	HS66110	EST89449	Homo sapiens	4.67e-10
	39	25	6.2	309	12	H27953	y162c09.r1	Homo sapie	4.67e-10
	40	25	6.2	362	17	H44273	yp17c03.r1	Homo sapie	4.67e-10
	41	25	6.2	362	117	HS273234	yp17c03.r1	Homo sapie	4.67e-10
	42	25	6.2	434	87	T93178	ye24e07.r1	Homo sapie	4.67e-10
	43	25	6.2	446	53	R71741	yj95dl1.r1	Homo sapie	4.67e-10
	44	25	6.2	471	17	H45128	yo66f01.r1	Homo sapie	4.67e-10
	45	25	6.2	471	114	HS128238	yo66f01.r1	Homo sapie	4.67e-10

ALIGNMENTS

RESULT 1 T27609 287 bp mRNA EST 06-SEP-1995  
LOCUS



DEFINITION	EST101034 Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJC regions (GB:M18512) (HT:3056).
ACCESSION	T27609
KEYWORDS	EST.
SOURCE	human primer=M13 Reverse library=Human Pancreas.
ORGANISM	Homo sapiens
	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choroanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 287)

REFERENCE AUTHORS	1 (bases 1 to 287)	TITLE	JOURNAL
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.M., Fitzgerald, L.M., FitzHugh, W.M., Friedman, J.L., Geoghagen, N.S.M., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Kline, K.M., Kelley, J.F., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.	Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence	Unpublished (1995)	

Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: [tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org)  
For clone availability, additional sequence and expression  
information related to this EST, please contact the TIGR Database  
([tdbinfo@tdb.tigr.org](mailto:tdbinfo@tdb.tigr.org)).

NCBI gi: 609707	
Location/Qualifiers	
1..287	
/organism="Homo sapiens"	
/note="human"	
<1..>287	
mRNA	
BASE COUNT	62 a 77 c 85 g 60 t
ORIGIN	3 others

Query Match 24.7%; Score 100; DB 69; Length 287;  
Best Local Similarity 71.1%; Pred.No.1.46e-157;  
Matches 167; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Db	14	atgactggacctggaggtactctctctggtggcagcagccanagagccactccag	73
Qy	1	ATGGGATGAGGGGGATCTTTCTCTCTCTGTCAGGAAC	60
Db	74	gtgcacctgggtgcagctggggctgggtggaagaagcctgggocctcagtgaa	133
Qy	61	ATCCACTGCAGCAGCTTGGACCTGAGCTGATGAGCCTGGGGCTTCAGT	120
Db	134	tgcgaactcttgatataacgctctccacgactatatactacgtgattccacag	193

[illegible]

RESULT	2
ID	H5727609 standard; RNA; EST; 287 BP.
AC	T27609;
DT	12-JAN-1995 (Rel. 42, Created)
DD	07-SEP-1995 (Rel. 45, Last updated, Version 3)
DE	EST101034 Homo sapiens cDNA 5' end similar to immunoglobulin mu
DE	heavy chain, VDJC regions (GB:M18512) (HT:3056).
DE	EST.
KW	Homo sapiens (human)
OC	Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC	Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.
RN	[1]
RP	1-287
RA	Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
RA	Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
RA	White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
RA	Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
RA	Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,
RA	Glocke A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,
RA	Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,
RA	Merrick J.M.; MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
RA	Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
RA	Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
RA	Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
RA	Coleman T.A., Collins E.J., Dimke D., Feng P., Ferlie A.,
RA	Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
RA	Gruber J., Hudson P., Kim A., Kosak D.L., Kunsch C., Ji H., Li H.,
RA	Melissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
RA	Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
RA	Haeletine W.A., Fields C., Frazer C.M., Venter J.C.;
RT	"Initial Assessment of Human Gene Diversity and Expression
RL	Patterns Based Upon 52 Million Basepairs of cDNA Sequence";
RL	Unpublished.
CC	Contact: Venter, JC The Institute for Genomic Research 932 Clopper
CC	Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:
CC	tbfinfo@db.tigr.org For clone availability, additional sequence
CC	and expression information related to this EST, please contact the
CC	TIGR Database ( <a href="mailto:tbfinfo@db.tigr.org">tbfinfo@db.tigr.org</a> ). NCBI gi: 609707
FH	Key Location/Qualifiers

FT	source	1..287	/organism="Homo sapiens"
FT			/note="human"
FT	mRNA	<1..>287	
SQ	Sequence	287 BP; 62 A; 77 C; 85 G; 60 T; 3 other;	

	Query Match	24.7%;	Score 100;	DB 127;	Length 287;
	Best Local Similarity	71.1%;	Pred. No. 1.46e-157;		
	Matches 167;	Conservative	0;	Mismatches 68;	Indels 0; Gaps
Db	14	atggactgagacctggaggatcctcttcttggtggcagcagccanaggagcccactccccag	73		
Qy	1	ATGGGATGGAGCGGGGATCTTTCTCTTCTCTGTGCAGAACTCAGGCTGCCACTTCGAC	60		
Db	74	gtgcacactggtgcagtcctggggcgtaggtgaagaagcctgggggocctcagtgaaggtctccc	133		
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Jul 8 08:37

US-08-137-117B-26.rst

5

QY 61 ATCCAGCTGCACGACTGTGACCTGACCTGATCAAGGCTGGGGCTTCAGTGAAGATATCC 120

Db 134 tqcaagactctggatcagcctccaccgactactatatacactgattcgacagccct 193  
||||| ||||| ||| ||||| ||| || ||||| ||| ||| |||

QY 121 TCGAAGGCTTCGGTTACTCATTCCTAGCTATTACATACATCTGGGTGAAGCAGGCAT 180

Db 194 gqacaaggcttgatggatggatgaacccctcgagtggtgcacaaact 248  
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QY 181 GCAAGAGCGCTGAGTGGATGATATTTGATCCTTCAATGGTGGTACTAGCT 235

RESULT 3

ID HS67011 standard; RNA; EST; 238 BP.

AC T29670;

DT 09-JAN-1995 (Rel. 42, Created)

DT 08-SEP-1995 (Rel. 45, Last updated, Version 2)

DE EST89669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy

DE chain V region (GB:X61012) (HT:3230).

RW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

RC [1]

RP 1-238

RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

RA Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,

RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,

RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,

RA Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,

RA Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,

RA Kelley J.M., Klinek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,

RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,

RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,

RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,

RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,

RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,

RA Meisner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,

RA Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,

RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;

RT "Initial Assessment of Human Gene Diversity and Expression

RT Patterns Based Upon 52 Million Basepairs of cDNA Sequence";

RL Unpublished.

CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper

CC Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:

CC tdbinfo@tdb.tigr.org For clone availability, additional sequence

CC and expression information related to this EST, please contact the

CC TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 611768

FH Key Location/Qualifiers

FH

FT source

FT 1..238

FT /organism="Homo sapiens"

FT /note="human"

FT mRNA

FT <1..>238

SQ Sequence 238 BP; 46 A; 70 C; 69 G; 52 T; 1 other;

Query Match 23.5%; Score 95; DB 122; Length 238;

Best Local Similarity 74.0%; Pred. No. 9.24e-147;

Matches 145; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Db 43 atggactggacctggagcatccttttntgtgtgcagcagcaacaggtgccactccag 102  
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QY 1 ATGGATGGACGGGATCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60

Jul 8 08:37

US-08-137-117B-26.rst

6

Db 103 gttaagcttggtgcagctgtgagctgaggtgaagcctggggcctcagtgaggtctcc 162  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 ATCCAGCTGCAGCAGCTGCGACCTGAGCTGATGAGCCTGGGGCTTCAGTGAAGATATCC 120

Db 163 tqcaagcttctggttacacccctttaccagctacggtatcagctgggtgcacagccct 222  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 TCGAAGGCTTCGGTTACTCATTCAGCTATTACATACACTGGGTGAAGCAGGCAT 180

Db 223 gqacaaggcttgagt 238  
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QY 181 GMAAGAGCGCTTGAGT 196

RESULT 4

LOCUS T29670 238 bp mRNA EST 06-SEP-1995

DEFINITION EST89669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy

chain V region (GB:X61012) (HT:3230).

ACCESSION T29670

KEYWORDS EST.

SOURCE human primer=M13 Reverse library=Human Small intestine.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 238)

AUTHORS Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,

White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W.,

Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,

Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,

Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,

Kelley J.M., Klinek K.M., Kelley J.C., Liu L.-I., Marmaros S.M.,

Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,

Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,

Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,

Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,

Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,

Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M.,

Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,

Meisner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C.,

Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,

Haseltine W.A., Fields C., Fraser C.M. and Venter J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns

Based Upon 52 Million Basepairs of cDNA Sequence

Unpublished (1995)

CONTACT: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database

(tdbinfo@tdb.tigr.org).

NCBI gi: 611768

Location/Qualifiers

1..238

/organism="Homo sapiens"

/note="human"

<1..>238

FEATURES

source

mRNA

BASE COUNT	46 a	70 c	69 g	52 t	1 others
ORIGIN					

Query Match 23.5%; Score 95; DB 70; Length 238;  
Best Local Similarity 74.0%; Pred. No. 9.24e-147;  
Matches 145; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Db 43 atgactggacctggagcatcctttnttggtgcagcagcaacagggtgccactcccg 102  
||||| |||| | |||| | |||| | |||| | |||| | |||| | ||||  
Qv 1 ATGGGATGGACGGGATCTTCTCTCTCTCTCTGTGCAGGAAGTCGAGGTGCCACTCTGAG 60

Db 103 gttcagctggtgcagtctggagctgagtggaagaagcctggggcgctcagtgaaggtctcc 162  
- - - - -  
Qw 61 ATCCAGCTGCAGCAGTCTGGACCTGACTGTAAGCCCTGGGGTTTCAGTGAAGATATCC 120

Db 163 tgcaaggcttctggttacacctttaccagctacggtatcagctgggtgcacagggccct 222  
|||||  
Ov 121 tgcraagcttctgggtactcattactagctattcatatacttgggtgaacagagccat 180  
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Db 223 ggacaaggccttgagt 238  
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Ov 181 ccaaacaccccttcaat 196

RESULT 5  
TO uc03011 standard. DNA. EST. 200 bp

AC T28938;  
 DT 08-JAN-1995 (Rel. 42, Created)  
 DT 07-SEP-1995 (Rel. 45, last updated, Version 2)  
 DE EST61186 Homo sapiens cDNA 5' end similar to immunoglobulin mu  
 heavy chain, VDJ regions (GB:MI7751) (HT:3055).  
 KW EST.

OC	homo sapiens (human)
OC	Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC	Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RP	(1)
RP	1-209
RA	Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,  
RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,  
RA FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geohagen N.S.M.,

RA Kellogg H., Elmwood Overly, Hanna (Mrs.) Newcomb Ltd., Hanna Co. Ltd.,  
RA Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmatos S.M.,  
RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,  
RA Pellerino S.M., Phillips C.A., Ryder S.E., Scott J.L.,  
RA

RA Sauer D.N., Smiley R., Smiley R.V., Spriggs I.R., Utterback I.R.,  
RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,  
RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,  
RA Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,

RA Gruber J., Hudson P., Kim A., Rozak D.L., Rusch C., Yi H.,  
RA Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,  
RA Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,  
RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.,

RT Patterns Based Upon 52 Million Basepairs of cDNA Sequence";  
 RL Unpublished.  
 CC Contact: Venter, JC The Institute for Genomic Research, 932 Clanner

CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC

tdinfo@tigr.org For clone availability, additional sequence  
and expression information related to this EST, please contact the  
TIGR database ([tdinfo@tigr.org](mailto:tdinfo@tigr.org)) or write to:  
Dr. Gaitanaris, MD 20878 Tel: 3018699036 Fax: 3018699423 Email:

FH	Key	Location/Qualifiers
FH		

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FT source 1..209
FT /organism="Homo sapiens"
FT /note="human"
FT mRNA <1..>209
FT SQ Sequence 209 BP; 43 A; 62 C; 48 G; 55 T; 1 other;

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Best Local Similarity 71.9%; Pred. No. 9,47e-132;  
Matches 143; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Db  
3 gatgtnccctggtaatggtgactctgccctggactctotgtaaataatttgtgttacca 62  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Cp  
281 GATTGTCAACAGCTCAATCTGGCCCTTGCCTTGAAATTCTGGTTGTAAGTACTACACCA 222

[illegible]

**D**b      123 tgcataagcatagttaggaagggtgatatccagaagccttgacggaaaccttcactgagacc 182  
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**C**p     161 TGATGTGTAATAGCTTAGTGCATTGGAAACCAAGAAGCCTTCGACGGATACTCCACTGAAGCC 102

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Db 183 ccaggcttcttcacatcag 201
      ||||| ||| |||||
Cc 101 CCAGCTTTCATCAGCTCAG 83

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RESULT	6	m20030	200 bp	DNA	EST	06 SEP 1995
LOCUS						

DEFINITION	EST61186 Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJ regions (GB:M17751) (HT:3055).
ACCESSION	T28938
FEATURES	com

SOURCE	ORGANISM
human primer=M13 Reverse Library=Human White blood cells.	Homo sapiens
	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

REFERENCE  
1 (bases 1 to 209)  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
Sarcotrypa; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

Bult, C. J., Lee, N., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White, O., Sutton, G., Blake, J. A., Brandon, R. C., Chiu, M.-W., Clayton, R. A., Cline, R. T., Cotton, M. D., Earle-Hughes, J., Fine, L. D.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancques, R.F., McDonald, L.A., Nguyen, D.T.,

Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,

Gruber, J., Hudson, P., Kim, A., Kozak, D. L., Kunsch, C., Li, H., Li, H.,  
Meissner, P. S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,  
Yu, G.-L., Ruben, S. M., Dillon, P. J., Fannon, M. R., Rosen, C. A.,

**TITLE** Initial Assessment of Human Gene Diversity and Expression Pattern Based Upon 52 Million Basepairs of cDNA Sequence

**JOURNAL** Unpublished (1995)

Contact: Venter, JC  
The Institute for Genomic Research  
932 Clippor Rd, Gaithersburg, MD 20878

Tel: 3018699056  
Fax: 3018699423  
Email: [tdbinfo@db.tigr.org](mailto:tdbinfo@db.tigr.org)  
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database ([tdbinfo@db.tigr.org](mailto:tdbinfo@db.tigr.org)).

		NCBI gi: 611036			
FEATURES	Location/Qualifiers				
source	1..209	/organism="Homo sapiens"			
		/note="human"			
mRNA	<1..>209				
BASE COUNT	43 a	62 c	48 g	55 t	1 others
ORIGIN					

Query Match 21.7%; Score 88; DB 70; Length 209;  
Best Local Similarity 71.9%; Pred. No. 9.47e-132;  
Matches 143; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Db           3   gatgntccctggtaatgggtgactctgccctggaactctgtaaaatttttgtgtacca   62  
            ||| |||     |||   |||   |||||       |||   |||   |||  
Cp          281   GATTGTCAACACTCAATGTGGCCCTGCCCTGAATTCCTGGTGTACTAGTACCACCA   222

Db 63 ttgccaggttgatccatcccatccactcaagcctttgtccgggggacctggcgacaccaa 122  
|||||  
Cp 221 TTGAAGGATCAATATATCCAACTCAAGGCTCTTTCCATGGCTGTGCTTCAACCCAG 162

D<sub>b</sub>    123   tgcatagcatagtagtgaagtgatccagaagccttcagaaacotttactgaggcc   182  
         |||         |||||         |         |||||         |||||         |||         |||         |||         |||  
  
C<sub>p</sub>    161   TGTATGTAATAGCTAGTGAATAGATAACCAAGAAGCCTTCAGAGATATTCTTCACTGAAGCC   102

Db 183 ccaggcttcttcacctcag 201  
||||| ||| |||||  
Cp 101 CCAGGCTTCATCAGCTCAG 83

<b>RESULT</b>	<b>7</b>			
<b>LOCUS</b>		R86288	385 bp	mRNA EST
<b>DEFINITION</b>		ypl2e09.r1 Homo sapiens cDNA clone 187240 5' similar to gb.L02325 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN) ;.		

**KEYWORDS** EST. human clone=187240 library=Soares breast 3NbHst vector=pT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCGAAGCGGAGCGCCCTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Cnoanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 395)

REFERENCE

**REFERENCE**

**AUTHORS**

1 (bases 1 to 395)

Bacterley, R., Kohn, J., Farnsworth, C., Gagliardi, L., Romagnolo, H.,  
Hollier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hullman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Travaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and  
Wilson, R.

TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT  
 Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 323  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL ; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

```

NCBI gi: 944694
FEATURES             Location/Qualifiers
     source            1..385
                        /organism="Homo sapiens"
                        /clone="187240"
                        /note="human"
BASE COUNT           85 a 104 c 112 g 78 t 6 others
ORIGIN
Query Match          17.8%;   Score 72;   DB 58;   Length 385;
Best Local Similarity 70.5%;   Pred. No. 4.76e-98;
Matches 129; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

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Db  
67 tctgcttggtgtagctccaggtgcacactcccagggtcaggtngtcagctcggg 126  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qv  
23 TCTTCTTCTGTGAGGAACACTGCAGGTGCCACTTGATCCAGCTCGCAGCTGGAC 82

[illegible]

Db 187 tcagccaccactacatgcactgggtgctgcagagccctggacaaggattnagtggctg 246  
||| - | ||||| ||||||| ||| ||||| ||| ||||| |  
Qv 143 TCAC TAGCTATTATCATACACTGGGTTGAAGCAGGCCATGGAAAGAGCC-TTCAGTGGATT 201

Db	247	gga	249
Qy	202	GGA	204

RESULT	8	LOCUS	T27127	299 bp	mRNA	EST	06-SEP-1995
DEFINITION			T313874 Homo sapiens cDNA 5' end similar to immunoglobulin mu (gamma) heavy chain, V(I)DJC regions (HIT:3057).				

ACCESSION 127727  
EST.  
KEYWORDS  
SOURCE human primer=M13 Reverse library=Human Testis.  
ORGANISM Homo sapiens

Lunarijocae; Nematozoa; Lumbricidae; Bilateria; Occomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 299)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chui, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fiergald, L.M., Fitzhugh, W.M., Fritcham, J.L., Geoghagen, N.S.M., Glöckner, A., Gnehm, J.L., Hanna, M.C., Hedblom, E., Hinkle, J.P., S., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chui, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fiergald, L.M., Fitzhugh, W.M., Fritcham, J.L., Geoghagen, N.S.M., Glöckner, A., Gnehm, J.L., Hanna, M.C., Hedblom, E., Hinkle, J.P., S.

REFERENCE  
AUTHORS

Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanco, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

**TITLE** Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence

**JOURNAL** Unpublished (1995)

**COMMENT**

Contact: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

NCBI gi: 609825

**FEATURES** Location/Qualifiers

**source**

1..299

/organism="Homo sapiens"

/notes="human"

**mRNA**

<1..>299

**BASE COUNT** 61 a 84 c 82 g 68 t 4 others

**Query Match** 13.3%; Score 54; DB 69; Length 299;

**Best Local Similarity** 63.8%; Pred. No. 1.35e-61;

**Matches** 125; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

**Db** 35 ggtttcttctctctgtggtgcagctcccagatgggtctgtcccaggtgcagtgcaag 94

|| |||| || |||| |||| |||| |||| |||| || |||| |||| || |||| |||| ||

**Qy** 14 GGATCTTTCTCTCTCTCTGACGAACTGCAGGTGTCACACTCTGAGATCCAGCTGCAGC 73

**Db** 95 agtggggccaggactggtgaagccttcggagaccctgtccctcacctgcactgtctctg 154

|||| || || || || || || || || || || || || || || || || || || || || ||

**Qy** 74 AGCTGGAACCTGAGCTGATGAGCCTGGGCTTCAGTGAAGATATCTTGCAGCGCTTCTG 133

**Db** 155 gtggctccatcagtagttactactaggactggatcgagccagccccaggaaggaactgc 214

|||| || || || || || || || || || || || || || || || || || || || || ||

**Qy** 134 GTTACTATTCTAGCTAGCTATTACATACACTGGGTGAAGCAGAGCCATGGAAGACCTTG 193

**Db** 215 agtgattgggttatat 230

|||| || || || || || || || || || || || || || || || || || || || || ||

**Qy** 194 AGTGGATTGGATATAT 209

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**ID** HST27727 standard; RNA; EST; 299 BP.

**AC** T27727;

**DT** 12-JAN-1995 (Rel. 42, Created)

**DT** 07-SEP-1995 (Rel. 45, Last updated, Version 2)

**DE** EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu

**DE** (gamma) heavy chain, V(IV)DJC regions (HT:3057).

**KW** EST.

**OS** Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Primates; Haplothinii; Catarrhini; Homnidae.  
RN [1]  
RP 1-299  
RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,  
RA Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,  
RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,  
RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,  
RA FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,  
RA Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,  
RA Kelley J.M., Klinek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,  
RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,  
RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,  
RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,  
RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,  
RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,  
RA Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,  
RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,  
RA Meissner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C.,  
RA Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,  
RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;  
RT "Initial Assessment of Human Gene Diversity and Expression  
RT Patterns Based Upon 52 Million Basepairs of cDNA Sequence";  
RL Unpublished.

**CC** Contact: Venter, JC The Institute for Genomic Research 932 Clopper  
CC Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:  
CC tdbinfo@tdb.tigr.org For clone availability, additional sequence  
CC and expression information related to this EST, please contact the  
CC TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 609825  
FH Key Location/Qualifiers

**FT** source 1..299  
**FT** /organism="Homo sapiens"  
**FT** /note="human"

**FT** mRNA <1..>299

**SQ** Sequence 299 BP; 61 A; 84 C; 82 G; 68 T; 4 other;

**Query Match** 13.3%; Score 54; DB 127; Length 299;

**Best Local Similarity** 63.8%; Pred. No. 1.35e-61;

**Matches** 125; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

**Db** 35 ggtttcttctctctgtggtgcagctcccagatgggtctgtcccaggtgcagtgcaag 94

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**Qy** 14 GGATCTTTCTCTCTCTCTGACGAACTGCAGGTGTCACACTCTGAGATCCAGCTGCAGC 73

**Db** 95 agtggggccaggactggtgaagccttcggagaccctgtccctcacctgcactgtctctg 154

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**Qy** 74 AGCTGGAACCTGAGCTGATGAGCCTGGGCTTCAGTGAAGATATCTTGCAGCGCTTCTG 133

**Db** 155 gtggctccatcagtagttactactaggactggatcgagccagccccaggaaggaactgc 214

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**Qy** 134 GTTACTATTCTAGCTAGCTATTACATACACTGGGTGAAGCAGAGCCATGGAAGACCTTG 193

**Db** 215 agtgattgggttatat 230

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**Qy** 194 AGTGGATTGGATATAT 209

**RESULT** 10

**LOCUS** SSC1D10 330 bp RNA EST 30-AUG-1995

**DEFINITION** S.scrofa mRNA; expressed sequence tag (5'; clone cld10).

**ACCESSION** F14516

**KEYWORDS** diversity region; EST; expressed sequence tag; immunoglobulin;

immunoglobulin heavy chain; joining region; variable region.

Jul 8 08:37

US-08-137-117B-26.rst

13

SOURCE pig.  
ORGANISM Sus scrofa  
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Sarcopharygii; Mammalia; Eutheria; Artiodactyla;  
Suiformes; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 330)  
AUTHORS Winteroe, A.K., Fredholm, M. and Davies, W.  
TITLE Evaluation and characterization of a porcine small intestine cDNA library  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 330)  
AUTHORS Winteroe, A.K.  
TITLE Direct Submission  
JOURNAL Submitted (26-JUL-1995) to the EMBL/GenBank/DBJ databases.  
Winteroe A.K., The Royal Veterinary and Agricultural University,  
Department of Animal Science and Animal Health, Division of Animal  
Genetics, Bulowvej 13, 1870 Frederiksberg C, DENMARK  
COMMENT NCBI gi: 971726  
FEATURES  
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            /clone\_lib="directionally cloned cDNA in XLI-blue MRF"  
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BASE COUNT 71 a 77 c 104 g 76 t 2 others  
ORIGIN  
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Best Local Similarity 58.7%; Pred. No. 9.76e-56;  
Matches 166; Conservative 0; Mismatches 117; Indels 0; Gaps 0;  
Db 45 aggtgtccagggtgagagaaggtgtggagctgtgagaggcctggcgagcctggng 104  
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          111 1111 1111 11111111 11111111 11111111  
Qy 165 GGTGAGCAGGCCATGGNAGAGCCCTTGAGTGGATATATTGATCCTTTCAATGG 224  
Db 225 tagtacctactacagagctctgtggagggcgattccacctcccaagaacaactccca 284  
          1111111111 111111111111 11111111 11111111  
Qy 225 TGGTACTAGTACACCAACCAAAATTCAGGGCAAGCCACATTGACTGTTCGCAAAATCTTC 284  
Db 285 gaagcggcctatctgcaaatnaacagcctgagaacagaagac 327  
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RESULT 11  
ID SSCID10 standard; RNA; EST; 330 BP.  
AC F14516;  
DT 30-AUG-1995 (Rel. 45, Created)  
DT 30-AUG-1995 (Rel. 45, Last updated, Version 1)  
DE S.scrofa mRNA; expressed sequence tag (5'; clone cld10)  
KW diversity region; EST; expressed sequence tag; immunoglobulin;  
KW immunoglobulin heavy chain; joining region; variable region.  
OS Sus scrofa (domestic pig)

Jul 8 08:37

US-08-137-117B-26.rst

14

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
Theria; Eutheria; Artiodactyla; Suiformes; Suidae.  
RN [1]  
RP 1-330  
RA Winteroe A.K., Fredholm M., Davies W.;  
RT "Evaluation and characterization of a porcine small intestine cDNA  
library";  
RT Unpublished.  
RN [2]  
RP 1-330  
RA Winteroe A.K.;  
RT ;  
RL Submitted (26-JUL-1995) to the EMBL/GenBank/DBJ databases.  
RL Winteroe A.K., The Royal Veterinary and Agricultural University,  
Department of Animal Science and Animal Health, Division of Animal  
Genetics, Bulowvej 13, 1870 Frederiksberg C, DENMARK  
FH Key Location/Qualifiers  
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          /note="expressed sequence tag"  
SQ Sequence 330 BP; 71 A; 77 C; 104 G; 76 T; 2 other;  
Query Match 12.6%; Score 51; DB 129; Length 330;  
Best Local Similarity 58.7%; Pred. No. 9.76e-56;  
Matches 166; Conservative 0; Mismatches 117; Indels 0; Gaps 0;  
Db 45 aggtgtccagggtgagagaaggtgtggagctgtgagaggcctggcgagcctggng 104  
          ||||| 1111 1111 11111111 1111111111  
Qy 45 AGGTGTCCACTCTGAGATCCAGCTGCAGCAGTCTGGACCTGACGTGATGAGCGCTGGGGC 104  
Db 105 gtctctgagactctctgtgcgctctgtgattccaccttcagtgtaacctacattaactg 164  
          11 1111 111111 11111111 1111111111  
Qy 105 TTCAGTGAAGATATCTCGAAGGCTTCGTGTACTCATTCATCTAGCTATTACATACACTG 164  
Db 165 ggtccgcaagctccagggaaggctggagtggtgctggcgctattagtagtgcgtgg 224  
          111 1111 1111 11111111 11111111 11111111  
Qy 165 GGTGAGCAGGCCATGGNAGAGCCCTTGAGTGGATATATTGATCCTTTCAATGG 224  
Db 225 tagtacctactacagagctctgtggagggcgattccacctcccaagaacaactccca 284  
          1111111111 111111111111 11111111 11111111  
Qy 225 TGGTACTAGTACACCAACCAAAATTCAGGGCAAGCCACATTGACTGTTCGCAAAATCTTC 284  
Db 285 gaagcggcctatctgcaaatnaacagcctgagaacagaagac 327  
          11 111111 1111 1111111111 11111111  
Qy 285 CAGCAGCGCTACATGTCATCTCAGCAGCGCTGACATCTCGAGAC 327

RESULT 12  
LOCUS T64512 169 bp mRNA EST 20-FEB-1995  
DEFINITION yc24f06.r1 Homo sapiens cDNA clone 81635 5' similar to gb:M18512 IG  
HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);.  
ACCESSION T64512  
KEYWORDS EST.  
SOURCE human clone=81635 library=Stratagene lung (#937210)  
vector=pBluescript SK- host=SOJLR cells (kanamycin resistant)  
primer=M13RP1 Rsitel=EcoRI Rsite2=XhoI Normal lung tissue from a 72  
year old male. Cloned unidirectionally. Primer: Oligo dT. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:  
5'-CAATTTCGGCAGAC-3'; 3' adaptor sequence:  
5'-CTCGAGTATTTT-3'.

ORGANISM	Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.	

REFERENCE  
AUTHORS  
1 (bases 1 to 169)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,  
Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

**TITLE** WashU-Merck EST Project  
**JOURNAL** Unpublished (1995)

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Fax: 314 200 1010  
Email: est@watson.wustl.edu  
High quality sequence stops: 139  
Source: IMAGE Consortium, I.I.N.I.

This clone is available royalty-free through LLNL; contact the SOURCE IMAGE Consortium, LLNL, for further information.

```
NCBI gi: 673557
FEATURES
    source
        Location/Qualifiers
            1..169
                /organism="Homo sapiens"
                /clone="81635"
                /vector="puc19"
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Query Match 10.6%; Score 43; DB 79; Length 169;  
Best Local Similarity 70.3%; Pred. No. 1.53e-40;  
Matches 90: Conservative 0; Mismatches 36; Indels

Db	43	atggaactggacctggaggatcctcttcttggtgcagtagcaagnga-gcccactccacg	101
Ov	1	ATGGCATCGAGCGGCACTTTTCTCTCTCTGTCCAGGAACGTGCGGTCCTCCTCTCAG	60

**Db** 102 gtgcacctggtgcagtctggggctgagatgaggaaacctggcct--cagtgaagggtccc 160  
| | | | | | | | | | | | | | | | | | | | |  
**Ov** 61 ATCCAGCTGCACGACTGGACCTGAGCTGATCAAGCTGGGCTTCAGTGAAGATATCC 120

Db	161	tgccaggc	168
Ov	121	TGCAAGGC	128

RESULT	13				
LOCUS	R83139	303 bp	mRNA	EST	04-AUG-1995
DEFINITION	ypl1g03.r1 Homo sapiens cDNA clone 187156 5' similar to gb:M62726 IG HEAVY CHAIN V-III REGION (HUMAN);.				

R83139  
 EST.  
 human clone=187156 library=Soares breast 3NbHst vector=pT7T3D  
 (Pharmacia) with a modified polylinker host=DH10B (ampicillin  
 resistant) primer=M1381 Rstel=Not I Rsite2=Eco RI Adult human.  
 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCTAGCTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),

digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Patima Ronaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 303)

**AUTHORS**  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevaekis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

TITLE	JOURNAL	COMMENT
The WashU-Merck EST Project	Unpublished (1995)	

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
 High quality sequence stops: 111  
 Source: IMAGE Consortium. L1NL

This clone is available royalty-free through LINL; contact the IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.

FEATURES	source	NCBI gi: 928016	Location/Qualifiers
		1..303	/organism="Homo sapiens"
			/clone="187156"
			/note="human"
BASE COUNT	62 a	65 c	91 g
ORIGIN			76 t
			9 others

Query Match 10.6%; Score 43; DB 57; Length 303;  
Best Local Similarity 61.8%; Pred. No. 1.53e-40;  
Matches 102; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Db 98 aggtgtccagtgtcaggtgcagctgcaggagctctggggaggcgtggtccagcctgggag 157

Qy 45 AGGTGCCACTCTGAGATCCAGCTGCAGCAGTCTGGACCTGAGCTGATGAAGCTGGGC 104

Db 158 gtccctgagactctcctgtgcagcctctggattcaccttcagtgggtatggcaggcactg 217

QY 105 TTCAGTGAAGATATCCTGCAAGGCTTCTGGTACTCATTCCACTAGCTATTACATPACACTG 164

RESULT	14
LOCUS	H73816          419 bp     mRNA         EST        31-OCT-1995
DEFINITION	Yalib01.r1 Homo sapiens cDNA clone 214441 5' similar to gb:M62726 IG HEAVY CHAIN V-III REGION (HUMAN); .
ACCESSION	H73816
KEYWORDS	EST.
SOURCE	human clones=214441 primer=M13RpI library=Soares fetal liver spleen INFILS vector=pf7T3D (Pharmacia) with a modified polylinker



host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAGAAATAATTAAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homo sapiens  
Eukaryota; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 419)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)

## TITLE

Contact: Wilson RK

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 261  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL / contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

## FEATURES

source  
1..419  
/organism="Homo sapiens"  
/clone="214441"  
/note="human"  
mRNA  
91 a 100 c 116 g 102 t 10 others  
<1..>419

## BASE COUNT

ORIGIN

Query Match 10.6%; Score 43; DB 100; Length 419;  
Best Local Similarity 58.6%; Pred. No. 1.53e-40;  
Matches 146; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Db 27 ctggggggctccctgagactctctgtgagcgtctggattccacttcagtagctatggca 86

Qy 98 CTGGGGGCTTCAGTGAAGATATCTCGAAGGCTTCTGGTTACTCATTCAGTAGCTATTACA 157

Db 87 tgcaatgggtccgcaggctccaggcaagggtgagctgggtggcatttatacggtagt 146

Qy 158 TACACTGGGTGAAGCAGGCGATGGAAGAGCGCTTGAGTGATTGGATATATTGATCCTT 217

Db 147 atggaagtaataatactatgcagactcgtgaaggccgattccaccatctccagagaca 206

Qy 218 TCAATGGTGTACTAGCTACACAGCAAAATTCAGGCGAAGGCCCAATTGACTGTTGACA 277

Db 207 attccaagaacacgtgtatctgcaaatgaacagctgagagctgaggaacacggctgtgt 266

Qy 278 AATCTTCCACACACGCTTACATGCATCTCAGCAGCGCTGCATCTGAGCAGTCT 337

Db 267 attactgtg 275

Qy 338 ATTACTGTG 346

## RESULT

ID HS816226 standard; RNA; EST; 419 BP.

AC H73816;

DT 03-NOV-1995 (Rel. 45, Created)

DT 03-NOV-1995 (Rel. 45, Last updated, Version 1)

DE y81b01.r1 Homo sapiens cDNA clone 214441 5' similar to gb:M62726

DE IG HEAVY CHAIN V-III REGION (HUMAN);

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

RN [1]

RP 1-419

RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,

RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,

RA Trevaskis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;

RT "The WashU-Merck EST Project";

RL Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC est@watson.wustl.edu High quality sequence stops: 261 Source: IMAGE

CC Consortium, LNL This clone is available royalty-free through LNL

CC ; contact the IMAGE Consortium (info@image.lnl.gov) for further

CC information. NCBI gi: 1046750

FH Key

FH Location/Qualifiers

FT source

FT 1..419

FT /organism="Homo sapiens"

FT /clone="214441"

FT /note="human"

FT mRNA

FT <1..>419

SQ Sequence 419 BP; 91 A; 100 C; 116 G; 102 T; 10 other;

Query Match 10.6%; Score 43; DB 124; Length 419;

Best Local Similarity 58.6%; Pred. No. 1.53e-40;

Matches 146; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Db 27 ctggggggctccctgagactctctgtgagcgtctggattccacttcagtagctatggca 86

Qy 98 CTGGGGGCTTCAGTGAAGATATCTCGAAGGCTTCTGGTTACTCATTCAGTAGCTATTACA 157

Db 87 tgcaatgggtccgcaggctccaggcaagggtgagctgggtggcatttatacggtagt 146

Qy 158 TACACTGGGTGAAGCAGGCGATGGAAGAGCGCTTGAGTGATTGGATATATTGATCCTT 217

Db 147 atggaagtaataataactatgcagactcgtgaaggccgattccaccatctccagagaca 206

Qy 218 TCAATGGTGTACTAGCTACACCAAGCAAAATTCAGGCGAAGGCCCAATTGACTGTTGACA 277

Db 207 attccaagaacacgtgtatctgcaaatgaacagctgagagctgaggaacacggctgtgt 266

Qy 278 AATCTTCCACACACGCTTACATGCATCTCAGCAGCGCTGCATCTGAGCAGTCT 337

Db 267 attactgtg 275

Qy 338 ATTACTGTG 346

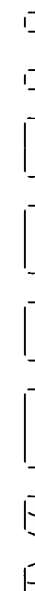
Jul 8 08:37

US-08-137-117B-26.rst

19

Search completed: Mon Jul 8 08:47:49 1996  
Job time : 199 secs.

(T4)



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protein - protein database search, using Smith-Waterman algorithm

```
Run on: Mon Jul 8 08:30:11 1996; MasPar time 7.52 Seconds
453.526 Million cell updates/sec
```

Tabular output not generated.

Title: >US-08-137-117B-27

Description: (1-135) from US08137117B.ppt

Perfect Score: 989

Sequence: 1 MGWSGIFLFLSGTAGVHSE.....ARGGNRFAYWGQCTLVTVSA 135

Scoring table: PAM 150

Gap 11

Searched: 82306 seqs, 25270970 residues

Post-processing: Minimum Match 0%

### Listing first 45 summaries

Database: pir46

1: ann1 2: ann2 3: ann3 4: unann1 5: unann2 6: unann3 7: unann4  
8: unann5 9: unann6 10: unann7 11: unann8 12: unrev1  
13: unrev2

Statistics: Mean 40.986: Variance 126.476: scale 0.324

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	809	81.8	137	5	H32513		Ig heavy chain precu	6.20e-89
2	808	81.7	135	5	P50057		Ig heavy chain precu	8.44e-89
3	777	78.6	474	13	S25057		Ig gamma-2b chain -	1.21e-84
4	771	78.0	139	5	A21609		Ig heavy chain precu	7.67e-84
5	769	77.8	138	5	S21810		Ig heavy chain V reg	1.42e-83
6	762	77.0	117	2	HWS8A		Ig heavy chain precu	1.23e-82
7	761	76.9	138	13	PH0105		anti-digoxin transefe	1.67e-82
8	744	75.2	135	5	A30577		Ig heavy chain precu	3.13e-80
9	743	75.1	150	5	PN0444		Ig heavy chain V reg	4.25e-80
10	740	74.8	141	5	JI0076		Ig heavy chain precu	1.07e-79
11	736	74.4	151	5	PL0011		Ig heavy chain precu	3.66e-79
12	726	73.4	469	11	S37483		Ig gamma-2a chain -	7.92e-78

Db 1 mqswifllsvtaqvhselqlqssgaelvkpqasvksckasqysftgynmnwvkqsh 60

## ALIGNMENTS

```

1
RESULT
ENTRY
  TITLE
  ORGANISM
  DATE
ACCESSIONS
REFERENCE
  #authors
  #journal
  #title
  #cross-references MWID:88331394
  #accession H32513
  ##molecule_type DNA
  ##residues 1-137 ##label KOF
CLASSIFICATION
  #superfamily immunoglobulin V region; immunoglobulin homology
  #length 137 #molecular-weight 15108 #checksum 816
SUMMARY
  Query Match 81.8%; Score 809; DB 5; Length 137;
  Best Local Similarity 82.5%; Pred. No. 6,20e-89;
  Matches 113; Conservative 13; Mismatches 9; Indels 2; Gaps 2;
Db 1 mqwswifllvtaqvhsqielqsgaetkvpqaeiskcasqsfyftgmnmwkvqsh 60

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Qy	1	MCWSGIFLFLLSGTAGVHSEIQQQSGPELMKPCASWKISCKASGSYFTSYIIHWKQSH	60
Db	61	gkolewignipnygsteynqkfkqkatltvdksstaymqhnlseedsavvyckany	120
Qy	61	gkslewiGYIDPNTGNGTSYNGKFKGKATLTVDKSSSTAYMHLSSLTSED	118
Db	121	gsesfdywgqgtltlves	137
Qy	119	GNRFAYWGQGLTVTVA	135
RESULT	2		
ENTRY	PS0057	#type complete	
TITLE	Ig heavy chain precursor V region (PAR) - mouse		
ORGANISM	#formal name Mus musculus #common name house mouse		
DATE	31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 12-Apr-1995		
ACCESSIONS	PS0057		
REFERENCE	PS0057		
#authors	Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.		
#journal	J. Biochem. (1988) 104:337-343		
#title	Biased expression of variable region gene families of the immunoglobulin heavy chain in autoimmune-prone mice.		
#cross-references	MUID:89197817		
#accession	PS0057		
	#molecule type DNA		
	#residues 1-135 #label YAO		
	#cross-references GB:D00307		
	#note the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly		
COMMENT	The gene encoding this protein was isolated from a hybridoma that produces anti-poly (ADP-ribose) antibody.		
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology immunoglobulin		
KEYWORDS			
FEATURE			
1-19	#domain signal sequence #label SIG		
20-135	#product Ig V region PAR #label MAT		
SUMMARY	#length 135 #molecular-weight 15019 #checksum 5383		
Query Match	81.7%; Score 808; DB 5; Length 135;		
Best Local Similarity	84.4%; Pred. No. 8.44e-89;		
Matches	114; Conservative 8; Mismatches 13; Indels 0; Gaps 0;		
Db	1	mqswliffllvttagvfeevqlqsgpeqlvkpgasvklscasqysftgyfmwvkqsh	60
Qy	1	MCWSGIFLFLLSGTAGVHSEIQQQSGPELMKPCASWKISCKASGSYFTSYIIHWKQSH	60
Db	61	gkolewigrinpyngdtfynqkfkqkatltvdksstahmelrlsleedsavvyckarly	120
Qy	61	gkslewiGYIDPNTGNGTSYNGKFKGKATLTVDKSSSTAYMHLSSLTSED	120
Db	121	rgaywgqgtltvtvea	135
Qy	121	RFAYWGQGLTVTVA	135
RESULT	3		
ENTRY	S25057	#type complete	
TITLE	Ig gamma-2b chain - mouse		
ORGANISM	#formal name Mus musculus #common name house mouse		
DATE	25-Feb-1994 #sequence_revision 25-Feb-1994 #text_change 25-Feb-1994		
ACCESSIONS	S25057		

```

REFERENCE      S25057
#authors      Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch,
               H.J.; Kreuzaler, F.
#submission   submitted to the EMBL Data Library, July 1992
#description   Production of a Tobacco mosaic virus (TMV) inactivating
               neotop specific monoclonal antibody in Nicotiana tabacum.
#accession    S25057
#status       preliminary
#residues     1-474 ##label FIS
##cross-references EMBL:X67210
SUMMARY       #length 474 #molecular-weight 52069 #checksum 4891

Query Match      78.6%; Score 777; DB 13; Length 474;
Best Local Similarity 77.4%; Pred. No. 1.21e-84;
Matches 106; Conservative 15; Mismatches 14; Indels 2; Gaps 2;

Db      1 mgwswiflllsgtagyhsveqlqsgpelvnpqasvkmcsckasgytfidymhwkqxp 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      1 MGWSGIFLLSQTAGVHSEIQLQSGPELMKPGASVKISCKASGYSTSYIHWVKQSH 60

Db      61 gqglwgiyinpndytsynqkfkgtatlvdksstaymqnlseedsavvyccarys 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      61 GKSLEWIGYIDPENGCTS VNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCARG-C 119

Db      121 ydwfaywgqgtlvtvesa 137
        ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      120 -NRFAYWGQGLTVTVSA 135

RESULT      4
ENTRY       A27609 #type complete
TITLE       Ig heavy chain precursor V region (I29) - mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change
            30-Sep-1993
ACCESSIONS  A27609
REFERENCE    A27609
#authors     Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
#journal     J. Immunol. (1988) 140:1676-1684
#title       I.29 lymphoma cells express a nonmutated V-H gene before and
            after H chain switch.
#cross-references MUID:88154467
#accession    A27609
#molecule type DNA
#residues     1-139 ##label KLE
##cross-references EMBL:M19401

GENETICS
#introns      16/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
1-19          #domain signal sequence #label SIG
20-139        #product Ig heavy chain V region I29 #label VAR
SUMMARY       #length 139 #molecular-weight 15643 #checksum 5928

Query Match      78.0%; Score 771; DB 5; Length 139;
Best Local Similarity 80.6%; Pred. No. 7.67e-84;
Matches 112; Conservative 13; Mismatches 10; Indels 4; Gaps 3;

Db      1 mgwswiflllsgtagyhsveqlqsgpelvnpqasvkmcsckasgytfidymhwkqsn 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      1 MGWSGIFLLSQTAGVHSEIQLQSGPELMKPGASVKISCKASGYSTSYIHWVKQSH 60

Db      61 gkslewgiyinpndytsynqkfkgtatlvdksstaymqnlseedsavvyccarys 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY      61 GKSLEWICYIDPNEGTSYNKQFKGATLTVDKSSSTAYMHLSSLTSEDSAVYYCARGN 120

Db      121 ysyvamydwqgtsvtvs 139
       : | ||||| |||||
QY      121 -RF-A--YWGGGLTVTSA 135

RESULT          5
ENTRY           Ig heavy chain V region - mouse
TITLE           #formal_name Mus musculus #common name house mouse
ORGANISM        20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
DATE            12-Apr-1995

ACCESSIONS     S2I810    #type complete
REFERENCE      S2I810    Ig heavy chain V region - mouse
               S2I811    #formal_name Mus musculus #common name house mouse
               Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
               Submitted to the EMBL Data Library, January 1991
               Nucleotide sequence of a rearranged VDJ-region of a mouse Ig
               mu heavy chain gene and its upstream region.
               #accession S2I810
               #status preliminary
               ##molecule_type DNA
               ##residues_ 1-138 #label OST
               ##cross-references EMBL:X56936

GENETICS
#introns       15/3
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY        #length 138 #molecular-weight 15258 #checksum 1535

Query Match      77.8%; Score 769; DB 5; Length 138;
Best Local Similarity 78.3%; Pred.No. 1,42e-83;
Matches 108; Conservative 11; Mismatches 16; Indels 3; Gaps 2;

Db      1 mgwstrifllsiaqhvcqqlqqsgpelvkpgasvriscskasyftfsyihwkvqrp 60
       ||| ||||| ||||| ::||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1 MGWSGIFLLSLTAGVISEIQQQSGELMKPGASVKISCKASGVFTSYIHWKQSH 60

Db      61 qgglewgiwypgnvntkynekfkgatltadkasstaymqslssedsavycarnyg 120
       |::||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      61 GKSLIEWIGYIDPNEGTSYNKQFKGATLTVDKSSSTAYMHLSSLTSEDSAVYYCARG-G 119

Db      121 syglaywgaggtlvtva 138
       : : ||||| |||||
QY      120 NRF--AYWGQGLTVTSA 135

```

```

RESULT      6
ENTRY       HVMS8A      #type complete
TITLE       Ig heavy chain precursor V region (108A) - mouse
            #formal_name Mus musculus #common_name house mouse
ORGANISM    18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change
            23-Mar-1995
DATE
ACCESSIONS  A02041
REFERENCE    A02041
            #authors    Cohen, J.B.
            Givol, D.; Zakut, R.; Efron, K.; Rechavi, G.; Ram, D.;
            Nature (1981) 292:426-430
            #journal
            #title       Diversity of germ-line immunoglobulin V-H genes.
            #cross-references MUID:81245215
            #accession   A02041
            #molecule_type DNA
            #residues    1-117 ##label GIV
            #note         the sequence was determined from the germline gene
            #superfamily Immunoglobulin V region; immunoglobulin homology
CLASSIFICATION

```

FEATURE	#domain signal sequence #status predicted #label SIG\
1-19	#product Ig heavy chain V region (108A) #status
20-117	predicted #label MATV
34-117	#domain immunoglobulin homology #label IMM
SUMMARY	#length 117 #molecular-weight 12971 #checksum 8923
Query Match	77.0%; Score 762; DB 2; Length 117;
Best Local Similarity	88.9%; Pred. No. 1.23e-82;
Matches 104; Conservative	8; Mismatches 5; Indels 0; Gaps 0;
Db	1 mgwswifllstgtagvhseqlqsgpselvkpgdskvskcasgtyftdynmhvkwsh 60
	:      :      :      :      :      :
Qy	1 MGSWGIFELLSGTAGVHSEIQLOQSPCLMKPGASVKISCKASGYSFTSYIHWKQSH 60
Db	61 gkslewigylypnynggtgynqtkfskatitvdnsststymesltsedssavyycar 117
	:      :      :      :      :      :
Qy	61 GKSLEWIGYIDPFNGGTSYNQKFKGKATITVDKSSSTAYMHLSSLTSEDSAVYICAR 117
RESULT 7	
ENTRY	PH0105 #type fragment
TITLE	anti-digoxin transfectoma antibody Light chain V region precursor - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	21-Nov-1993 #sequence_revision 21-Nov-1993 #text_change 21-Nov-1993
ACCESSIONS	PH0105
REFERENCE	PH0105
#authors	Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.; Haber, E.; Jacobson, M.A.; Mol. Immunol. (1990) 27:901-909
#journal	Heavy and light chain contributions to antigen binding in an
#title	anti-digoxin chain recombinant antibody produced by transfection of cloned anti-digoxin antibody genes.
#cross-references	MUID:91015092
#accession	PH0105
#status	preliminary
#residues	1-138 ##label NEA
SUMMARY	#length 138 #checksum 3011

```

Query Match      76.9%; Score 761; DB 13; Length 138;
Best Local Similarity 76.1%; Pred. No. 1.67e-82;
Matches 105; Conservative 18; Mismatches 12; Indels 3; Gaps 2;

Db 1 mgwewifllsntagvlsevqlqsgpel.vhpgkasvrmackssgysiftdfymnwvrqsh 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 MGNSSGIFPELLSGTAGVHSEIQLOQSGPELMPKPGASVKISCKASGVSFTSYVIHWKQSH 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 gksldyigvispysgvtgynqkfkgkatltvdksstaymelrsltsedsavycagsg 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 GKSLEWIGYIDPENGSTSNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCA-RGG 119
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 121 nkwmamydwhghqasvtsas 138
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 120 NRFA--YWCQGTLTVTWSA 135
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
ENTRY A30577 #type fragment
TITLE Ig heavy chain precursor V region (MRL10) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 04-May-1989 #sequence revision 04-May-1989 #text_change
12-Apr-1995

```

ACCESSIONS	REFERENCE
A30577	Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theofilopoulos, A.N.
A30577	J. Exp. Med. (1985) 161:805-815
#authors	Genetic elements used for a murine lupus anti-DNA autoantibody are closely related to those for antibodies to exogenous antigens.
#journal	
#title	

```

#cross-references MUID:85159423
#accession A30577
##status preliminary
##molecule_type mRNA
##residues 1-135 #label KOF
#cross-references GB:M37621
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 135 #checksum 8166

```

Query Match	75.2%;	Score 744;	DB 5;	Length 135;
Best Local Similarity	73.3%;	Pred. No. 3.13e-80;		
Matches	99;	Conservative	23;	Mismatches 13;
				Indels 0;
				Gaps 0;

1	mgwsciiiflvaatgvhgcvgqlqggaevlpqasvklackagvftfayvnnvkarp	60
Db		
1	mgwsciiiflvaatgvhgcvgqlqggaevlpqasvklackagvftfayvnnvkarp	60
Qy		
1	mgwsgiflflustgvgvhselqlqoqgpekmkpcasvklscragstfstsytihwvqsh	60
Db		
61	ggglewignipygsstnynekfkskatitvdtsastaymqslslatdcaavyccarlv	120
Qy		
61	gkslewigyidpfnngtstynokfkgatitvdksststaymhlslstsdsvavycargen	120

```

Db      121 gfaygggtlvtvs 135
      ++++++
Qv      121 RFAYWGOGTLVTSA 135

```

RESULT	9
ENTRY	PN0444
TITLE	Iq heavy chain V region precursor - human (fragment)
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 30-Sep-1993

ACCESSIONS	REFERENCE	#authors	#journal	#title
PN0444	Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U. H.	5	Gene (1992) 122:321-328	A general method for chimeraization of monoclonal antibodies by inverse polymerase chain reaction which conserves authentic N-terminal sequences.

```
#accession P00444
#molecule_type mRNA
#residues 1-150 ##label KAL
#cross-references GB:U02346
CLASSIFICATION ##superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
```

FEATURE	
1-19	#domain signal sequence #status predicted #label sig\
20-150	#product Ig heavy chain V region #status predicted #label MAT\
20-117	#domain variable region #label VRG
SUMMARY	#length 150 #checksum 9720

Query Match 75.1%; Score 743; DB 5; Length 150;  
Best Local Similarity 77.5%; Pred. No. 4.25e-80;  
Matches 107; Conservative 13; Mismatches 14; Indels 4; Gaps 3;

Db	1	mewswiflllsgtagvlsaeqlqqfgaelvbkpqtssvkisckaegyiftdymndmwwkqsh	60
		:  :	
Qy	1	MWSGIFLFLLSGTAGVHSEIQLQQSGPELMKPCASVKISCKASGYFTSYTIHWVKQSH	60
		:  :	
Db	61	gkslswigldipnfds-ssynqkfkgkatltvksntaymelsltsestavyycarg	119
		:  :	
Qy	61	GKSLIEWIGYIDP-FNGGTSYNQKFGKATLTVDKSSSTAYMLHSLTSEDSAVYYCARG	119
		:  :	
Db	120	fpygmcygqgqtsvtvss	137
		::	
Qy	120	NREA--YMGQGLTWVSA	135

RESULT	10
ENTRY	
TITLE	JL0076 #type fragment
	ig heavy chain precursor v region (anti-phenyloxazalone, 18C10) - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 12-Apr-1995

JL0076  
 JL0076  
 #authors Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.  
 #journal Mol. Immunol. (1988) 25:859-865  
 #title Combinatorial association of V genes: one VH gene codes for three non-cross-reactive monoclonal antibodies each specific for a different antigen (phOxalone, NP or GAT).  
 #cross-references MUID:89096973

```
#cross-references MUID:89096973
#accession JI0076
#molecule_type mRNA
#residues 1-141 ##label KAA
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
```

```

1-19
20-141
50-54
69-85
123-135
136-141
SUMMARY
#domain signal sequence #label SIG\
#product ig heavy chain #status predicted #label MAT\
#region complementarity-determining 1\
#region complementarity-determining 2\
#region J2 segment\
#region C
#length 141 #checksum 8784

```

Query Match 74.8%; Score 740; DB 5; Length 141;  
Best Local Similarity 73.3%; Pred. No. 1.07e-79;  
Matches 99; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

```

Db      1 mgwscimlflaatatgvhsqvlqpggaeivkpgasvklsckasgytftsyywmhwkqrp 60
      ||||| : :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Ov      1 MGWSGTFELLSGTAGVHSEIDLOOSPELMPGASVKTSCKASGYSETSYYIHWVKOSH 60

```

```
Db      61 grglewigrdnpnsggtkynrefkstatlvtvkpsstaymqslssltedsavvycaregp   120  
       (::::lll lll :ll ):::lll:l::::lll:l::::lll:l::::lll:l::::lll+l  
  
Ov     61 GKSLEWIGYIDPNNGGTSYNOREKFGATLTVDKSSSTAYMHLSSLTSDSVAVYCARGN    120
```

```

Db 121 agdywgggttltvss 135
      ||||| :|||
Ov 121 REAYWGOGTLVTVSA 135

```

RESULT	11
ENTRY	PL0011
TITLE	Ig heavy chain precursor V region (4C11) - mouse (fragment)
ORGANISM	#formal name Mus musculus #common name house mouse
DATE	30-Jun-1992 #sequence revision 30-Jun-1992 #text change

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28-Apr-1995  
 PL0011  
 Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.;  
 Kohler, H.  
 Mol. Immunol. (1988) 25:33-40  
 #title Structural basis of stimulatory anti-idiotypic antibodies.  
 #cross-references MJD:88142863  
 #accession PL0011  
 ##molecule\_type mRNA  
 ##residues 1-151 ##label CHE  
 ##experimental source cell line 4C11  
 ##COMMENT This protein is an anti-idiotypic antibody that induces an  
 anti-phosphorylcholine response.  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS immunoglobulin  
 FEATURE  
 1-19 #domain signal sequence #label SIG\

20-136 #product Ig heavy chain V region (4C11) #label MAT\

50-54 #region complementarity-determining 1\

69-85 #region complementarity-determining 2\

118-125 #region complementarity-determining 3\

137-151 #domain constant region #label COR

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Qy 1 MWSGIFLFLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSFTSYIHWVKQSH 60  
 Db 61 qggkwiqgfwipagntkynenfkqkatltvdtsstaymqlesleedtaayfcarang 120  
 Qy 61 GKSLEWIGYIDPENGSTYNQKFKGKATLTVDKSSSTAYMHLSLTSEDSAVYYCARG-G 119  
 Db 121 atatlldywgqgtstvtvs 139  
 Qy 120 NR---FAYWQGQTLTVSA 135

RESULT 13  
 ENTRY #type complete  
 TITLE Ig heavy chain V region (anti-anti-TNFAlpha Mab 1G3) - mouse  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 03-Mar-1995

ACCESSIONS S41429  
 REFERENCE S41429  
 #authors Saseano, M.; Repetto, M.; Casani, G.; Corti, A.  
 #submission submitted to the EMBL Data Library, January 1994  
 #description PCR amplification of antibody variable regions with primers  
 that anneal to constant regions.  
 #accession S41429  
 #status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-138 ##label SAS  
 ##cross-references EMBL:X77230  
 SUMMARY #length 138 #molecular-weight 15208 #checksum 9990

Query Match 73.1%; Score 723; DB 11; Length 138;  
 Best Local Similarity 76.8%; Pred. No. 1.99e-77;  
 Matches 106; Conservative 12; Mismatches 17; Indels 3; Gaps 3;

Db 1 mqwswifllqgtagvlavqlqsgpelvkpgasvkisckasgdfgtndlhvrqsh 60  
 Qy 1 MWSGIFLFLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSFTSYIHWVKQSH 60  
 Db 61 vrslewigrispyngvtvsnknfkdkatltvdtsstaymelheltseasvyyctptt 120  
 Qy 61 GKSLEWIGYIDPENGSTYNQKFKGKATLTVDKSSSTAYMHLSLTSEDSAVYYCAR-GG 119

Db 121 vdtwfwywgqgtclvtvsa 138  
 Qy 120 -N-RFAYWQGQTLTVSA 135

RESULT 14  
 ENTRY #type fragment  
 TITLE Ig heavy chain precursor V region (F6-3) - mouse (fragment)  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 11-Apr-1995

ACCESSIONS PL0012  
 REFERENCE PL0012  
 #authors Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.;  
 Kohler, H.  
 Mol. Immunol. (1988) 25:33-40  
 #title Structural basis of stimulatory anti-idiotypic antibodies.  
 #cross-references MJD:88142863  
 #accession PL0012  
 ##molecule\_type mRNA  
 ##residues 1-166 ##label CHE

Query Match 73.4%; Score 736; DB 5; Length 151;  
 Best Local Similarity 77.9%; Pred. No. 3.66e-79;  
 Matches 106; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

Db 1 mqwswifllqgtagvlavqlqsgpelvkpgasvkisckasgyftfdymhwkqsh 60  
 Qy 1 MWSGIFLFLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSFTSYIHWVKQSH 60  
 Db 61 gkalewigfdpnydnfynekfkdkatltvdtsstaymelrsletseasvyycaasyd 120  
 Qy 61 GKSLEWIGYIDPENGSTYNQKFKGKATLTVDKSSSTAYMHLSLTSEDSAVYYCARGG- 119

Db 121 galdywgqgtstvtvs 136  
 Qy 120 NREAYWQGQTLTVSA 135

RESULT 12  
 ENTRY #type complete  
 TITLE Ig gamma-2a chain - mouse  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

ACCESSIONS S37483  
 REFERENCE S37483  
 #authors Duncanson, F.F.D.  
 #submission submitted to the EMBL Data Library, February 1993  
 #accession S37483  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-469 ##label DUC  
 ##cross-references EMBL:X70423  
 SUMMARY #length 469 #molecular-weight 51549 #checksum 7833

Query Match 73.4%; Score 726; DB 11; Length 469;  
 Best Local Similarity 74.1%; Pred. No. 7.92e-78;  
 Matches 103; Conservative 15; Mismatches 17; Indels 4; Gaps 2;

Db 1 mqwswifllqgtagvhcqlqsgpelvkpgasvkisckasgyftfdymhwkqtp 60



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##experimental\_source cell line F6-3

COMMENT This protein is an anti-idiotypic antibody which induces an anti-phosphorylcholine response.

KEYWORDS immunoglobulin

FEATURE 1-32 #domain signal sequence #label SIG\  
33-151 #product Ig heavy chain V region (4C11) #label MAT\  
63-67 #region complementarity-determining 1\  
82-98 #region complementarity-determining 2\  
131-140 #region complementarity-determining 3\  
152-166 #domain constant region #label COR  
SUMMARY #length 166 #checksum 5824

Query Match 73.1%; Score 723; DB 11; Length 166;  
Best Local Similarity 73.9%; Pred. No. 1.99e-77;  
Matches 102; Conservative 17; Mismatches 16; Indels 3; Gaps 2;

Db 14 mqwswifllsagtagvlsqvlqgsgpelakpgasvkmackasgyrftdyvmhvwkqsn 73

QY 1 MCMWGIFLLSGTAGVHSEIQLQSGPELWKPGASVKISKASGYSTSYIHWKQSH 60

Db 74 gkalewigstnpyidytnykenfkgratvtvkssstvmqnlstsedsavvycaregg 133

QY 61 GKSLEWICYIDPPNGGTSYNQKFGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCAR--G 118

Db 134 fgnsldywgqgtvsnvs 151

QY 119 -GNRFAYWGQGLTVTVSA 135

RESULT 15

ENTRY S09216 #type complete

TITLE Ig heavy chain precursor - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995

ACCESSIONS S09216

REFERENCE S09216

#authors Okamoto, M.; Honjo, T.

#journal Nucleic Acids Res. (1990) 18:1895

#title Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoantibody produced by a hybridoma from NZB mouse.

#cross-references MUID:90245589

#accession S09216

##status preliminary

##molecule\_type mRNA

##residues 1-140 #label OKA

##cross-references EMBL:X51741

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

SUMMARY #length 140 #molecular-weight 15532 #checksum 3371

Query Match 72.8%; Score 720; DB 5; Length 140;

Best Local Similarity 71.9%; Pred. No. 5.00e-77;

Matches 97; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

Db 1 mewplisllsagtagvlsqvlqgsgaelvpgasvksckasgyafsedmwnlkrp 60

QY 1 MCMWGIFLLSGTAGVHSEIQLQSGPELWKPGASVKISKASGYSTSYIHWKQSH 60

Db 61 gkalewigqlypgdgtynnenfrdkatldkstvmqnlstsedsavvycargdy 120

QY 61 GKSLEWICYIDPPNGGTSYNQKFGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCARGN 120

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Db 121 wfpwgggtlvtvea 135

Qy 121 RFAYWGQGLTVTVSA 135

Search completed: Mon Jul 8 08:30:40 1996  
Job time : 29 secs.

(TM)

MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:29:44 1996; MasPar time 4.34 Seconds  
477.475 Million cell updates/sec

Tabular output not generated.

```
>US-08-137-117B-27
Title:
Description: (1-135) from US08137117B, pep
Perfect Score: 989
Sequence: 1 MGWSGIFLELLSGTGVHSE.....
```

Sequence: 1 MGWSGIFLFLSLGTAGVHSE.....ARGGNRFAYWGQGLVTVSA 135

Scoring table: PAM 150  
Gap 11

Searched: 43470 seqs, 15335248 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

```
Database: swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8
```

Statistics: Mean 41.703; Variance 74.406; scale 0.560

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	762	77.0	117		HV14_MOUSE	IG HEAVY CHAIN PRECUR	3.00e-144
2	719	72.7	139		HV07_MOUSE	IG HEAVY CHAIN PRECUR	2.40e-134
3	717	72.5	140		HV02_MOUSE	IG HEAVY CHAIN PRECUR	6.93e-134
4	706	71.4	137		HV11_MOUSE	IG HEAVY CHAIN PRECUR	2.34e-131
5	705	71.3	136		HV15_MOUSE	IG HEAVY CHAIN PRECUR	3.96e-131
6	698	70.6	138		HV48_MOUSE	IG HEAVY CHAIN PRECUR	1.60e-129
7	681	68.9	118		HV51_MOUSE	IG HEAVY CHAIN V REGI	1.27e-125
8	677	68.5	117		HV12_MOUSE	IG HEAVY CHAIN V REGI	1.05e-124
9	675	68.3	117		HV13_MOUSE	IG HEAVY CHAIN V REGI	3.01e-124
10	675	68.3	117		HV52_MOUSE	IG HEAVY CHAIN PRECUR	3.01e-124
11	671	67.8	117		HV49_MOUSE	IG HEAVY CHAIN PRECUR	2.48e-123
12	668	67.5	117		HV04_MOUSE	IG HEAVY CHAIN PRECUR	1.21e-122
13	665	67.2	117		HV06_MOUSE	IG HEAVY CHAIN PRECUR	5.87e-122

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3

Qy 1 MWGSGIFLLSGTAGVHSEIQSQSGPELMPKPGASVKISCKASGYFTSYIHWKQSH 60  
 Db 61 qkalewlgvipyngqgtgynqgkfkakatlvdnssstaymelselstedsaavycar 117  
 Qy 61 GKSLEWIGYIDFNGGTSYNQKFKGKATLVDKSSSTAYMHLSSLTSEDSAVYCAR 117

RESULT 2  
 ID HV07 MOUSE STANDARD; PRT; 139 AA.  
 AC P01751; P01752;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RM 81234548  
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,  
 RA BALTIMORE D.;  
 RL CELL 24:625-637(1981).  
 CC -/- THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING  
 CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB  
 CC ANTIBODIES).  
 DR PIR; A02034; MHMS18.  
 DR HSP; P01810; 1JHL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT CHAIN 1 19  
 FT DOMAIN 20 139 IG HEAVY CHAIN V REGION (B1-8 / 186-2).  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 65 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 86 117 FRAMEWORK 3.  
 FT DOMAIN 118 124 D SEGMENT.  
 FT DOMAIN 125 139 JH2 SEGMENT.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON TER 139 139  
 SQ SEQUENCE 139 AA; 15419 MW; 118806 CN;

Query Match 72.7%; Score 719; DB 4; Length 139;  
 Best Local Similarity 71.9%; Pred. No. 2.40e-134;  
 Matches 100; Conservative 21; Mismatches 14; Indels 4; Gaps 3;

Db 1 mgwscimflaatqvhsgvqlqpgaeivkpgasvklsckasgyftsyimhwkqrp 60  
 Qy 1 MWGSGIFLLSGTAGVHSEIQSQSGPELMPKPGASVKISCKASGYFTSYIHWKQSH 60  
 Db 61 qkalewlgvipyngqgtgynqgkfkakatlvdnssstaymelselstedsaavycar 120  
 Qy 61 GKSLEWIGYIDFNGGTSYNQKFKGKATLVDKSSSTAYMHLSSLTSEDSAVYCAR-G- 118

RESULT 3  
 ID HV02 MOUSE STANDARD; PRT; 140 AA.  
 AC P01746;

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DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/J;  
 RM 82152818  
 RA SIMS J., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,  
 RA CAPRA J.D.;  
 RL SCIENCE 216:309-311(1982).  
 DR PIR; A02028; HVMSG7.  
 DR HSP; P01789; 6FAB.  
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYBRIDOMA; SIGNAL.  
 FT SIGNAL 1 19  
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).  
 FT NON TER 140 140  
 SQ SEQUENCE 140 AA; 15514 MW; 116859 CN;

Query Match 72.5%; Score 717; DB 4; Length 140;  
 Best Local Similarity 73.6%; Pred. No. 6.93e-134;  
 Matches 103; Conservative 19; Mismatches 13; Indels 5; Gaps 2;  
 Db 1 mgwscimflaatqvhsgvqlqpgaeivkpgasvklsckasgyftsyimhwkqrp 60  
 Qy 1 MWGSGIFLLSGTAGVHSEIQSQSGPELMPKPGASVKISCKASGYFTSYIHWKQSH 60  
 Db 61 qkalewlgvipyngqgtgynqgkfkakatlvdnssstaymelselstedsaavycar 120  
 Qy 61 GKSLEWIGYIDFNGGTSYNQKFKGKATLVDKSSSTAYMHLSSLTSEDSAVYCAR--- 117  
 Db 121 ygseyfdywgqgtltvs 140  
 Qy 118 -GGR-FAYWGQGLTVTSA 135

RESULT 4  
 ID HV11 MOUSE STANDARD; PRT; 137 AA.  
 AC P01755;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (S43).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RM 81234548  
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,  
 RA BALTIMORE D.;  
 RL CELL 24:625-637(1981).  
 CC -/- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING  
 CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB  
 CC ANTIBODIES).  
 DR PIR; A02038; G2MS43.  
 DR HSP; P01772; 1EGV.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 19  
 FT CHAIN 20 137 IG HEAVY CHAIN V REGION (S43).  
 FT DOMAIN 20 49 FRAMEWORK 1.

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FT	DOMAIN	50	54	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	55	68	FRAMEWORK 2.
FT	DOMAIN	69	85	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	86	117	FRAMEWORK 3.
FT	DOMAIN	118	122	D SEGMENT.
FT	DOMAIN	123	137	JH2 SEGMENT.
FT	DISULFID	41	115	BY SIMILARITY.
FT	NON TER	137	137	
SQ	SEQUENCE	137 AA;	15200 MW;	108780 CN;
Query Match 71.4%; Score 706; DB 4; Length 137;				
Best Local Similarity 69.3%; Pred. No. 2.34e-131;				
Matches 95; Conservative 25; Mismatches 15; Indels 2; Gaps 2;				
Db	1	mgwscimiflaatatgthgqvclqqpgaefvfpqasvklackasgytftslmhwnqrp	60	
		: : :     : : :     : : :     : : :     : : :     : : :		
Qy	1	MWSGIFLLSLGAGVHSEIQAGSGPELMKPGAVKISKACSGYSFTSYIHWWKQSH	60	
Db	61	grglewigrdpsngggttynehrsksatltdkpsstaymqlesltseavyyccaryl	120	
		:          : : :     : : :     : : :     : : :     : : :     : : :		
Qy	61	GKSLIEWIGYIPDPNGGTSYNQKFKATLTVDKSSSTAYMHLSSLTSEDSAVYYCAR	119	
Db	121	grfydyggggttltsv	137	
		f         :     :		
Qy	120	NR-FAYWGQGLTVTVA	135	

RESULT	5	
ID	HV15 MOUSE	STANDARD; PR7; 136 AA.
AC	P01759;	
DT	21-JUL-1986	(REL. 01, CREATED)
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)
DT	01-FEB-1991	(REL. 17, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN	PRECURSOR V REGION (BC11).
OS	MUS MUSCULUS	(MOUSE).
OC	EUKARYOTA;	METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA;	RODENTIA.
RN	[1]	
RP	SEQUENCE FROM N.A.	
RM	82222262	
RA	KNAPP M.R., LIU C.-P.,	NEWELL N., WARD R.B., TUCKER P.W., STROBER S.,
RA	BATTNER F.R.;	
RL	PROC. NATL. ACAD. SCI. U.S.A.	79:2996-3000(1982).
DR	EMBL; J00494;	MMIGHAQ.
DR	PIR; A02042;	HVMSB1.
DR	HSSP; P01789;	IJEL.
KW	IMMUNOGLOBULIN V REGION;	SIGNAL.
FT	SIGNAL	1 19
FT	CHAIN	20 136 IG HEAVY CHAIN V REGION (BC11).
FT	NON TER	136 136
SQ	SEQUENCE	136 AA; 115078 MW; 110014 CN;

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Query Match      71.3%; Score 705; DB 4; Length 136;
Best local Similarity 70.6%; Pred. No. 3.96e-131;
Matches 96; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

Db      1 mgwscilflvatatgshsqvqlqsgqgsvrvrpgvsvkiskcgsgyftdyamhwkvqsh 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      1 MGWSGILFLLSGTAGVHSEIQLOQSGPELMLKPGASVKISCKASGYSTSYIIHWKQSH 60

Db      61 akslewigistvngnteynqdfkfatmtvdkasestvhmelarltsedsanlycaryvg 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      61 GKSLEWIGIDYDPFGNGTSYNQKFKGATLVDKSSSTAYVHLLSLTSDSVAYYCARG-G 119

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Db	121	nyfaywggattltvss	136
		:    :	
Qy	120	NRfAYWGQTIWTVSA	135
RESULT 6			
ID	HV48	MOUSE STANDARD; PRT; 138 AA.	
DT	P03980;		
DT	23-OCT-1986	(REL. 02, CREATED)	
DT	23-OCT-1986	(REL. 02, LAST SEQUENCE UPDATE)	
DT	01-AUG-1992	(REL. 23, LAST ANNOTATION UPDATE)	
DE	IG	HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).	
OS	MUS	MUSCULUS (MOUSE).	
OC	EUKARYOTA;	METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA;	RODENTIA.	
RN	[1]		
RP	SEQUENCE FROM N.A.		
RM	84248078		
RA	GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,		
RA	TUCKER P.W.;		
RL	PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168 (1984).		
DR	PIR; A02033; HVMST7.		
DR	HSP; P01810; LOHL.		
KW	IMMUNOGLOBULIN V REGION; SIGNAL.		

Query Match 70.6%; Score 698; DB 4; Length 138;  
Best Local Similarity 68.1%; Pred. No. 1.60e-129;  
Matches 94; Conservative 25; Mismatches 16; Indels 3; Gaps 2;

Db	1	mgsyailflvatatdvhvqlqpgaelvkpgasvqlskaeghtftnywhvwkqp	60
		:    :    :    :    :    :    :    :    :    :    :	
Qy	1	MGSGIFLLSCTAGVHSEIQLQQSGPELMKPGASYKISCKASGYFTSYTHWVKQS	60
		:    :    :    :    :    :    :    :    :    :    :	
Db	61	qgglewgieipndgrsyneknkatltvdksastaymqlesltpfefavvycazad	120
		:    :    :    :    :    :    :    :    :    :    :	
Qy	61	GKSLEIGYIDPENGSTYNOKFKRATLTVDKSSSTAYMHLSSLTSDSAVYVCARG-G	119
		:    :    :    :    :    :    :    :    :    :    :	
Db	121	ywdfywgqgtlvtfesa	138
		::	
Qy	120	--NRFAWGQGLTVTVA	135

RESULT	7	
ID	HV51 MOUSE	STANDARD; PRT; 118 AA.
AC	P06330;	
DT	01-JAN-1988	(REL. 06, CREATED)
DT	01-JAN-1988	(REL. 06, LAST SEQUENCE UPDATE)
DT	01-MAR-1992	(REL. 21, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN V REGION	(AC38 205.12).
OS	MUS MUSCULUS	(MOUSE).
OC	EUKARYOTA; METAZOA;	CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.	

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RN SEQUENCE.
RM 84182519
RA DILDROP R., BOVENS J., STEKEVITZ M., BEYREUTHER K., RAJESKY K.;
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01772; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 85344 CN;

Query Match 68.9%; Score 681; DB 4; Length 118;
Best Local Similarity 81.4%; Pred. No. 1.27e-125;
Matches 96; Conservative 10; Mismatches 10; Indels 2; Gaps 2;

Db 1 evqlqsgpelvkgasvknscasgytfdymwkvqshgkslewigdnpnngttsy 60
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 EIQLQSGPELMKPGASVKISCKASYFTSYIHWVKQSHGKSLIEWIGYIDPFNGGTSY 79

Db 61 nqkfkgkatltvdksatymqlnsltsedsavvyccardryfdwaggtttvss 118
+|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVVYCARG-G-NRPAYWGQGLTVTUSA 135

RESULT 8
ID HV12 MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (MOPC 104E).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 83075344
RA KERRY M.R., FUHRMAN J.S., SCHILLING J.W., ROGERS J., SIBLEY C.H.,
RA HOOD L.E.;
RL BIOCHEMISTRY 21:5415-5424(1982).
CC -|- THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS
CC ALSO BEEN DETERMINED.
CC -|- THIS PROTEIN BINDS DEXTRAN.
DR HSP; A02039; MHMS4E.
DR HSSP; P01772; IFGV.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 82832 CN;

Query Match 68.5%; Score 677; DB 4; Length 117;
Best Local Similarity 81.2%; Pred. No. 1.05e-124;
Matches 95; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

Db 1 evqlqsgpelvkgasvknscasgytfdymwkvqshgkslewigdnpnngttsy 60
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 EIQLQSGPELMKPGASVKISCKASYFTSYIHWVKQSHGKSLIEWIGYIDPFNGGTSY 79

Db 61 nqkfkgkatltvdksatymqlnsltsedsavvyccardryfdwaggtttvss 117
+|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
SQ SEQUENCE 117 AA; 12983 MW; 82832 CN;

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Qy 80 NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVVYCARGNR-FAYWGQGLTVTUSA 135
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
ID HV13 MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (J558).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 80078170
RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;
RL NATURE 283:35-40(1980).
CC -|- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN
CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN
CC THE D AND J SEGMENTS.
CC -|- THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; ZFGW.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 82647 CN;

Query Match 68.3%; Score 675; DB 4; Length 117;
Best Local Similarity 81.2%; Pred. No. 3.01e-124;
Matches 95; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

Db 1 evqlqsgpelvkgasvknscasgytfdymwkvqshgkslewigdnpnngttsy 60
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 EIQLQSGPELMKPGASVKISCKASYFTSYIHWVKQSHGKSLIEWIGYIDPFNGGTSY 79

Db 61 nqkfkgkatltvdksatymqlnsltsedsavvyccardryfdwaggtttvss 117
+|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVVYCARGNR-FAYWGQGLTVTUSA 135
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
ID HV52 MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH558 A1/A4).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RM 85099340
RA YANCOPOULOS G.D., ALT F.W.;
RL CELL 40:271-281(1985).
DR EMBL; M13787; MWIGHVA.
DR PIR; A02029; HWSA1.
DR HSSP; P01772; IFOR.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH558 A1/A4).

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FT	DOMAIN	20	49	FRAMEWORK 1.
FT	DOMAIN	50	54	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	55	68	FRAMEWORK 2.
FT	DOMAIN	69	85	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	86	117	FRAMEWORK 3.
FT	DISULFID	41	115	BY SIMILARITY.
FT	NON TER	117	117	
SQ	SEQUENCE	117 AA;	12971 MW;	77250 CN;

Query Match 68.3%; Score 675; DB 4; Length 117;  
Best Local Similarity 78.6%; Pred. No. 3.01e-124;  
Matches 92; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

[illegible][illegible]

Query Match	67.8%;	Score 671;	DB 4;	Length 117;
Best Local Similarity	75.2%;	Pred. No. 2.48e-123;		
Matches	88;	Conservative 18;	Mismatches 11;	Indels 0;
			Gaps 0;	

[illegible]

RESULT	12
ID	HV04 MOUSE STANDARD; PRT; 117 AA.
AC	P01748;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN PRECURSOR V REGION (23).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6;
RM	81234548
RA	BOTHELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,
RA	BALTIMORE D.;
RL	CELL 24:625-637(1981).
CC	-! THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC	THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR	PIR; A02030; HWMS23.
DR	HSP; P01810; IJHL.
KW	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL 1 19
FT	CHAIN 20 117 IG HEAVY CHAIN V REGION (23).
FT	DOMAIN 20 49 FRAMEWORK 1.
FT	DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 55 68 FRAMEWORK 2.
FT	DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 86 117 FRAMEWORK 3.
FT	DIVELFD 41 115 BY SIMILARITY.
FT	NON TER 117 117
SO	SEQUENCE 117 AA: 12772 MW: 80102 CN:

Query Match	67.5%;	Score 668;	DB 4;	Length 117;
Best Local Similarity	75.2%;	Pred. No. 1.21e-122;		
Matches	88;	Conservative 18;	Mismatches 11;	Indels 0; Gaps 0;

D6	1	mgeciillfvaangvhoqvqlgqpgtelvlpgsaevklckeaagtfsyemhwkvkqp	60
		:     :     :     :     :     :     :     :	
Q7	1	MGWSGIIFLFLSGTAGVHEIQIQQSQPELMKPGASVKISCKAGSYFTSIYHWKQSH	60
		:     :     :     :     :     :     :     :	
D6	61	ggglwlginpngnngnynekfkektvlvdksastayqlssltedsavvyccar	117
		:     :     :     :     :     :     :     :	
O9	61	GKSLEITGVIPENGGTSYNOKFKCATLVDKSSTAYMHLSSLTSDSVAVYYCAR	117
		:     :     :     :     :     :     :     :	

RESULT	13
ID	HV06 MOUSE STANDARD; PRT; 117 AA.
AC	P01750;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN PRECURSOR V REGION (102).
OS	MUS MUSCULOUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.
RN	[1]
RC	SEQUENCE FROM N.A. STRAIN=C57BL/6;
RM	81234548
RA	BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K BALTIMORE D. ;
RL	CELL 24; 625-637(1981).





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US-08-137-117B-27.rag

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W P S R E H

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:30:57 1996; MaxPar time 4.67 Seconds  
Tabular output not generated. 239.615 Million cell updates/sec

Title: >US-08-137-117B-27  
Description: (1-135) from US08137117B.pep  
Perfect Score: 989  
Sequence: 1 MGWSGIFILSLGTAGVHSE.....ARGNRFAYWGQTLTVWSA 135

Scoring table: PAM 150  
Gap 11

Searched: 70887 seqs, 8282111 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneeq22  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14

Statistics: Mean 29.935; Variance 137.631; scale 0.218

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	986	99.7	135	6	R28669 p12-h2.	1.27e-78
2	807	81.6	137	12	R62445 R1C6 heavy chain vari	3.43e-62
3	796	80.5	137	10	R53330 KM-750 heavy chain.	3.48e-61
4	790	79.9	139	10	R53328 KM-796 heavy chain.	1.23e-60
5	786	79.5	135	6	R29017 pUC-RVh-1220d.	2.86e-60
6	784	79.3	135	6	R29016 pUC-RVh-1220b.	4.35e-60
7	780	78.9	137	1	R05090 Heavy chain variable	1.01e-59
8	763	77.1	141	2	R12356 Heavy chain variable	3.61e-58
9	762	77.0	135	2	R24107 Humanised anti-Fac an	4.46e-58
10	759	76.7	135	2	R06369 Anti-Fac heavy chain	8.38e-58
11	759	76.7	140	2	R12334 Mouse MAb 2G12 H chai	8.38e-58
12	758	76.6	144	2	R08346 Heavy chain variable	1.03e-57

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13	745	75.3	140	10	R55554 DREG-200 Ab heavy cha	1.59e-56
14	742	75.0	138	8	R39266 Mouse C4G1 Ig heavy-c	2.99e-56
15	740	74.8	140	5	R09425 Co-1 Heavy Chain V Re	4.55e-56
16	739	74.7	134	1	R06250 Variable region of mu	5.61e-56
17	739	74.7	136	2	P70624 Sequence encoded by a	5.61e-56
18	733	74.1	135	1	P93151 Protein encoded by V	1.98e-55
19	731	73.9	139	7	R38259 Chimeric 128.1 VH, mo	3.01e-55
20	731	73.9	233	7	R41710 Murine 128.1 VH/human	3.01e-55
21	731	73.9	235	7	R41707 Murine 128.1 VH/human	3.01e-55
22	731	73.9	235	7	R41715 Murine 128.1 VH/human	3.01e-55
23	731	73.9	235	7	R41682 Cimeric antibody comp	3.01e-55
24	726	73.4	136	10	R59512 Sequence of the heavy	8.61e-55
25	726	73.4	469	8	R40384 Monoclonal antibody M	8.61e-55
26	720	72.8	143	14	R84554 MAb SCH94.03 heavy ch	3.03e-54
27	720	72.8	163	3	R15060 Murine anti-ICAM mono	3.03e-54
28	720	72.8	163	3	R15200 R6-5-D6 anti-ICAM-1 h	3.03e-54
29	719	72.7	137	2	R12360 Heavy chain variable	3.74e-54
30	719	72.7	137	2	R12238 Mouse MAb 4D12 H chai	3.74e-54
31	717	72.5	136	1	R04133 Anti-Leu 3a heavy cha	5.69e-54
32	712	72.0	139	7	R33950 CTM01 VH.	1.63e-53
33	707	71.5	134	7	R38311 Sequence of murine an	4.64e-53
34	700	70.8	139	6	R29009 p64-h2 protein produc	2.01e-52
35	699	70.7	114	4	R21271 Murine VH group 1 cha	2.48e-52
36	699	70.7	153	2	R11597 Murine monoclonal 14.	2.48e-52
37	696	70.4	143	2	R12233 Mouse MAb 2E12 H chai	4.66e-52
38	696	70.4	144	2	R12355 Heavy chain variable	4.66e-52
39	693	70.1	136	10	R59510 Sequence of the heavy	8.74e-52
40	687	69.5	134	1	R04383 Colon Cancer monoclon	3.07e-51
41	685	69.3	134	7	R38312 Sequence of murine an	4.67e-51
42	684	69.2	141	5	R09427 ME4 Heavy Chain V Reg	5.76e-51
43	684	69.2	468	3	R13061 Monoclonal antibody O	5.76e-51
44	683	69.1	136	1	R04382 Colon Cancer monoclon	7.10e-51
45	682	69.0	140	5	R27049 VH425 antibody cloned	8.76e-51

#### ALIGNMENTS

RESULT 1	ID	R28669	standard; Protein; 135 AA.
AC	R28669;		
DT	30-MAR-1993	(first entry)	
DE	p12-h2.		
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;		
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;		
KW	plasmid; p12-k2; p12-h2.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT	/note= "Signal peptide"		
FT	Protein	20..135	
FT	/note= "Mature peptide"		
PN	W09219759-A.		
PD	12-NOV-1992.		
PF	24-APR-1992; J00544.		
PR	25-APR-1991; JP-095476.		
PR	19-FEB-1992; JP-032084.		
PA	(CHUS ) CHUGAI SEIYAKU KK.		
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Teuchiya M;		
DR	WPI; 92-398882/48.		
DR	N-PSDB; Q30754.		
PT	Reconstituted human antibody to human interleukin-6 receptor -		
PT	has low antigenicity and contains mouse V-region complementarity		
PT	determining regions		
PS	Disclosure; Page 119-20; 207pp; Japanese.		

[illegible]

Db 1 mgwswifllsqtavlsevqlqqsg

Db 1 mgswwifllsgtagvlsevlqsggpelvkpgasvkiackasgytftdynamdwkqsh 60

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QY 1 MGWGFIFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSFTSYTHWVKQSH 60  
 Db 61 qkswlgiyypnnggtgynqkfkkatltvdksstaymelhsltsedavvyatagr 120  
 QY 61 GKSLWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSITSSEDSAVVYCARGN 120  
 Db 121 yyyawdgqgtltvtvsa 137  
 QY 121 RF-AV-WGQGLTIVTSA 135  
 RESULT 4  
 ID R53328 standard; Protein; 139 AA.  
 AC R53328;  
 DE 17-NOV-1994 (first entry)  
 KW Monoclonal antibody; Ab; ganglioside GM2; chimera;  
 KW chimeric antibody; expression vector; heavy; light; chain;  
 KW hypervariable region; CDR; constant region; hybridoma;  
 KW Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= sig\_peptide  
 FT Region 50..54  
 FT /label= CDR1  
 FT /note= "claim 8"  
 FT Region 69..85  
 FT /label= CDR2  
 FT /note= "claim 8"  
 FT Region 118..128  
 FT /label= CDR3  
 FT /note= "claim 8"  
 PN A09346181-A.  
 PD 17-MAR-1994.  
 PF 07-SEP-1993; 046181.  
 PR 07-SEP-1992; JP-238452.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;  
 PI Shitara K;  
 DR WPI; 94-126857/16.  
 DR N-PSDB; Q45426.  
 PT Humanised antibody specific for ganglioside GM2 - used for  
 PT producing a cytotoxic effect on cancers such as melanoma,  
 PT neuroblastoma and glioma.  
 PS Claim 5; Page 104-105; 191pp; English.  
 CC Chimeric human Ab expression vectors are constructed by inserting  
 CC the Ab heavy and light chain variable region-encoding cDNA  
 CC isolated from hybridomas producing a mouse or rat monoclonal Ab  
 CC reacting with the ganglioside GM2 respectively into an expression  
 CC vector for use in animal cells which contains the human Ab heavy and  
 CC light chain constant region-encoding cDNA. The expression vectors  
 CC are introduced into animal cells and the transformant thus obtained  
 CC is cultured for the prodn. of a chimeric human Ab reacting with the  
 CC ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric  
 CC human Abs will not cause anti-mouse Ig Ab prodn. in the patient's  
 CC body but show a prolonged blood half-life, with a reduced frequency  
 CC of adverse effects, so that it can be expected to be superior  
 CC to mouse monoclonal Abs in the efficacy in the treatment of human  
 CC cancer, for instance.  
 CC Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603  
 CC heavy and light chain sequences are given in Q45426-30.  
 CC CDR regions for use in chimeric Abs are indicated in the

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CC Features Table.  
 SQ Sequence 139 AA;  
 Query Match 79.9%; Score 790; DB 10; Length 139;  
 Best Local Similarity 84.2%; Pred. No. 1.23e-60;  
 Matches 117; Conservative 6; Mismatches 12; Indels 4; Gaps 2;  
 Db 1 mgwswiflllsgtagvlsqvlgqsgpeelvkpgasvkiackasgyftdymdwvkqsh 60  
 QY 1 MGWGFIFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSFTSYTHWVKQSH 60  
 Db 61 qkswlgiyypnnggtgynqkfkkatltvdksstaymelhsltsedavvyatagyh 120  
 QY 61 GKSLWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSITSSEDSAVVYCAR-G- 118  
 Db 121 yyyawdgqgtltvtvsa 139  
 QY 119 --GNRFAYWGQGLTIVTSA 135  
 RESULT 5  
 ID R29017 standard; Protein; 135 AA.  
 AC R29017;  
 DT 30-MAR-1993 (first entry)  
 DE pUC-RVh-1220d.  
 KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;  
 KW complementarity determining region; monoclonal; hybridoma; PCR;  
 KW plasmid; polymerase chain reaction; amplify.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "Leader peptide"  
 FT Region 20..49  
 FT /label= FR1  
 FT Region 50..54  
 FT /label= CDR1  
 FT Region 55..68  
 FT /label= FR2  
 FT Region 69..85  
 FT /label= CDR2  
 FT Region 86..117  
 FT /label= FR3  
 FT Region 118..124  
 FT /label= CDR3  
 FT Region 125..135  
 FT /label= FR4  
 PN W09219759-A.  
 PD 12-NOV-1992.  
 PF 24-APR-1992; J00544.  
 PR 25-APR-1991; JP-095476.  
 PR 19-FEB-1992; JP-032084.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 DR WPI; 92-398882/48.  
 DR N-PSDB; Q31391.  
 PT Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 PS Disclosure; Page 159-60; 207pp; Japanese.  
 CC The sequences given in R29016-17 are portions of monoclonal antibodies  
 CC which were encoded by plasmids contained within the mouse hybridoma,  
 CC AUK12-20. The DNA encoding the complementarity determining regions  
 CC (CDR's) was isolated by polymerase chain reaction. These antibodies  
 CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells







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```

Db      1 mewsgvifllsvtasvhsqvlqsgaelvgpgtsvrsvcskasgafntyliewkwqrp 60
      1 |||:|||| |||:|||||:|: |||:|||||:|: |||:|||||:|: |||
Qv      1 MGVSGIFLFLSGTAGVHSEIQQQSGPELMKPGCASVKISCKASGVSFTSYIHWKQSH 60

```



**RESULT** 15

Query Match 74.8%; Score 740; DB 5; Length 140;  
Best Local Similarity 77.1%; Pred. No. 4.55e-56;  
Matches 108; Conservative 12; Mismatches 15; Indels 5; Gaps 3;

Db	1	mewswiflllsgtaghsevlqqsgpelvtpgasyvmckasgyftfsvnmhwkdkp	60
		:     :     :     :     :     :     :     :     :     :	
Qy	1	MGSSGIFLLSLSGTAGVHSEIQLQQSGPELMKPGASVKISCKASGYFTSYIHWKQSH	60
		:     :     :     :     :     :     :     :     :	
Db	61	qgglwgiyipyndgtsynpeffgkatltcdkssastameleeltdesavvyccariy	120
		:     :     :     :     :     :     :     :     :	
Qy	61	GKSLIEWIDYDPNGGTSYNQKFKGKATLVDSKSTAYMHLSLTSDESAVYICARGG-	119
		:     :     :     :     :     :     :     :     :	
Db	121	fdysyvmwygqggtvrtvas	140
		: :      :	
Qy	120	-N-RFA--YWGQGTLTVTSA	135

Search completed: Mon Jul 8 08:31:25 1996  
Job time : 28 secs.



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3

Best Local Similarity 92.9%; Pred. No. 2.52e-89; Matches 118; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 msaqflgllllcfqgtrcdtqttslsaslgdrvtiscrasqdiynylnwyqkdp 60  
Qy 1 msaqflgllllcfqgtrcdtqttslsaslgdrvtiscrasqdiynylnwyqkdp 60  
Db 61 dgtvkllyvtrhsqgvrfsqsgtdysltisnlegediatyfcqgntlpwtfgg 120  
Qy 61 dgtvkllyvtrhsqgvrfsqsgtdysltisnlegediatyfcqgntlpwtfgg 120  
Db 121 gtlkleik 127  
Qy 121 gtlkleik 127

RESULT 2  
ENTRY A26406 #type complete  
TITLE Ig kappa chain V region (Ara-A) - mouse  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 30-Jun-1989 #sequence\_revision 30-Jun-1991 #text\_change 12-Apr-1995  
ACCESSIONS A26406  
REFERENCE A26406  
#authors Sanz, I.; Capra, J.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:1085-1089  
#title V-K and J-K gene segments of A/J Ara-A antibodies: somatic recombination generates the essential arginine at the junction of the variable and joining regions.  
#cross-references MUID:871147197  
#accession A26406  
#molecule type DNA  
#residues 1-128 ##label SAN

##cross-references GB:M15519  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 128 #molecular-weight 14078 #checksum 4901

Query Match 95.5%; Score 868; DB 5; Length 128;  
Best Local Similarity 92.9%; Pred. No. 2.43e-88;  
Matches 118; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 1 msaqflgllllcfqgtrcdtqttslsaslgdrvtiscrasqdiynylnwyqkdp 60  
Qy 1 msaqflgllllcfqgtrcdtqttslsaslgdrvtiscrasqdiynylnwyqkdp 60  
Db 61 dgtvkllyvtrhsqgvrfsqsgtdysltisnlegediatyfcqgntlpwtfgg 120  
Qy 61 dgtvkllyvtrhsqgvrfsqsgtdysltisnlegediatyfcqgntlpwtfgg 120  
Db 121 gtlkleik 127  
Qy 121 gtlkleik 127

RESULT 3  
ENTRY A34904 #type complete  
TITLE Ig kappa chain precursor V region (5-27) - mouse  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 12-Apr-1995  
ACCESSIONS A34904  
REFERENCE A34903  
#authors Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
#journal J. Biol. Chem. (1990) 265:133-138

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#title Active site structure and antigen binding properties of idiotypically cross-reactive anti-fluorescein monoclonal antibodies.  
#cross-references MUID:90094387  
#accession A34904  
#status preliminary; not compared with conceptual translation  
#molecule\_type mRNA  
#residues 1-126 ##label BED

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 126 #molecular-weight 13839 #checksum 3586

Query Match 94.8%; Score 862; DB 5; Length 126;  
Best Local Similarity 93.7%; Pred. No. 1.33e-87;  
Matches 118; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 1 msaqflgllllcfqgtrcdtqttslsaslgdrvtiscrasqdiynylnwyqkdp 60  
Qy 2 VSSAQFLGILLLCFQGTCTCDTQTTSLSASLGDRVTISCRASQDISSYLNWYQKDP 61  
Db 61 gtvkllyvtrhsqgvrfsqsgtdysltisnlegediatyfcqgntlpwtfgg 120  
Qy 62 gtvkllyvtrhsqgvrfsqsgtdysltisnlegediatyfcqgntlpwtfgg 121  
Db 121 tklein 126  
Qy 122 tklein 127

RESULT 4  
ENTRY A29380 #type fragment  
TITLE Ig kappa chain precursor V region (AC-1001) - mouse (fragment)  
ORGANISM #formal name Mus musculus #common name house mouse  
DATE 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 12-Apr-1995  
ACCESSIONS A29380  
REFERENCE A29380

#authors Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
#journal J. Biol. Chem. (1987) 262:13579-13583  
#title Nucleotide and translated amino acid sequences of cDNA coding for the variable regions of the light and heavy chains of mouse hybridoma antibodies to blood group A and B substances.

#cross-references MUID:88007582  
#accession A29380  
#molecule\_type mRNA  
#residues 1-122 ##label CHE  
#note the authors translated the codon TTC for residue 1 as Leu  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
SUMMARY #length 122 #checksum 9064

Query Match 91.5%; Score 832; DB 5; Length 122;  
Best Local Similarity 94.2%; Pred. No. 6.50e-84;  
Matches 114; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 1 flgllllcfqgtrcdtqttslsaslgdrvtiscrasqdiynylnwyqkdpvkl 60  
Qy 7 FUGLLLCFQGTCTCDTQTTSLSASLGDRVTISCRASQDISSYLNWYQKDPDTIKL 66  
Db 61 lihyterlshqgvrfsqsgtdysltisnlegediatyfcqgntlpwtfggtklei 120  
Qy 67 LIYTSRLHSGVPSRFSGSGTDSYLTINNLEQDIATYFCQGNLTLPYTFGGTKLEI 126

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Db 121 k 121  
Qy 127 N 127

RESULT 5

ENTRY A53276 #type complete  
TITLE immunoglobulin kappa variable chain - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 28-Apr-1995

ACCESSIONS A53276

REFERENCE A53276

#authors Kim, S.O.; Sanz, I.; Williams, C.; Capra, J.D.; Gottlieb, P.D.

#journal Immunogenetics (1991) 34:231-241

#title Polymorphism in V kappa 10 genes encoding L chains of antibodies bearing the Ar-A and A48 cross-reactive idiotypes.

#cross-references MUID:92010099

#accession A53276

##status preliminary

##molecule\_type DNA

##residues 1-115 #label KIM

##cross-references NCBI:62777; NCBI:62780

##experimental\_source AJL strain

##note #sequence extracted from NCBI backbone

SUMMARY #length 115 #molecular\_weight 12681 #checksum 7342

Query Match 88.9%; Score 808; DB 11; Length 115;

Best Local Similarity 96.5%; Pred. No. 5.74e-81;

Matches 111; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 mmsaefglililcfqgtrcdiqmtqtsslaslgdrvtiscrasqdiynylnwyqktp 60

Qy 1 MVSSAQFGLGLLCCQGTTCIDQMTQTSSLASLGDRVTISCRASQDISSYLNWYQKPK 60

Db 61 dgtvkllyytrlhsgvprfsgsgtdytslnleqediatyfcqgntlp 115

Qy 61 DGTIKLLIYYSRLHSGVPSRFSGSGCTDYSITINNLEQEDIATYFCQGNLTLP 115

RESULT 6

ENTRY JL0080 #type fragment

TITLE Ig light chain precursor V region (anti-phenylloxazolone, 18C10) - mouse (fragment)

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 12-Apr-1995

ACCESSIONS JL0080

REFERENCE JL0076

#authors Kaartinen, M.; Rocca-Serra, J.; Maekela, O.

#journal Mol. Immunol. (1988) 25:859-865

#title Combinatorial association of V genes: one VH gene codes for three non-cross-reactive monoclonal antibodies each specific for a different antigen (phOxazolone, NP or CAT).

#cross-references MUID:89096973

#accession JL0080

##molecule\_type mRNA

##residues 1-115 #label KAA

##note the authors translated the codon AGG for residue 30 as Ser

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

FEATURE

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1-6 #domain signal sequence (fragment) #label SIG\  
7-115 #product Ig light chain #status predicted #label MAT\  
30-40 #region complementarity-determining 1\  
56-62 #region complementarity-determining 2  
SUMMARY #length 115 #checksum 7375

Query Match 86.7%; Score 788; DB 5; Length 115;

Best Local Similarity 96.5%; Pred. No. 1.63e-78;

Matches 109; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 fggtrcdiqmtqtsslaslgdrvtiscrasqdiynylnwyqkpdgtvkllyytsrl 60

Qy 15 FQGTTCIDQMTQTSSLASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYYSRL 74

Db 61 hsgvprfsgsgtdytslnleqediatyfcqgntlpvtfgggtkleik 113

Qy 75 HSGVPSRFSGSGCTDYSITINNLEQEDIATYFCQGNLTLPVTFGGGTKEIN 127

RESULT 7

ENTRY S19970 #type fragment

TITLE Ig kappa chain V region (M-Ti51) - mouse (fragment)

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 12-Apr-1995

ACCESSIONS S19970

REFERENCE S19963

#authors Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

#description submitted to the EMBL Data Library, March 1992

#accession S19970

##status preliminary

##molecule\_type mRNA

##residues 1-108 #label WEI

##cross-references EMBL:X65095

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

SUMMARY #length 108 #checksum 2135

Query Match 79.3%; Score 721; DB 5; Length 108;

Best Local Similarity 92.5%; Pred. No. 2.52e-70;

Matches 99; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 1 dlqmtqtsslaslgdrvtiscrasqdiynylnwyqkpdgtvkllyytsrlhsgvps 60

Qy 21 DIQMTQTSSLASLGDRVTISCRASQDISSYLNWYQKPDGTIKLLIYYSRLHSGVPS 80

Db 61 rfsgsgtdytslnleqedvatyfcqgntlpvtfgggtkleik 107

Qy 81 RFSGSGTDYSLTINNLEQEDIATYFCQGNLTLPVTFGGGTKEIN 127

RESULT 8

ENTRY B28044 #type complete

TITLE Ig kappa chain V region (GP1) - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 12-Apr-1995

ACCESSIONS B28044

REFERENCE A94179

#authors Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.

#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248

#title Identity of the V-kappa-10-Are-A gene segments of the A/J and BALB/c strains.

#cross-references MUID:87317629

```

#accession B28044
#molecule_type mRNA
#residues 1-107 ##label MEE
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
#length 107 #molecular-weight 11738 #checksum 7011
SUMMARY

```

Query Match	78.5%;	Score 714;	DB 5;	Length 107;
Best Local Similarity	94.4%;	Pred. No. 1.80e-69;		
Matches 101;	Conservative 5;	Mismatches 1;	Indels 0;	Gaps 0;

Db 1 diqmtqttesleaslgdrvaiscrasqdianynwvqqkpdgtvklllyytsrlhsqvps 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 21 DIQMOTQTSSLASLGRVATISCRASQDISSVLNWWQQKPDGTIKLLIYTSRLHSQVPS 80

Accession	Protein	Length	Score	E-value
61	rfsagsgt dysalt is nleqedi at yfcggnt l prtfgggt kkleik	107	127	0.000000
QV	81 RFSGSGGWDYSLTINNLEEDIATYFCOOGNTLPYTFGGGTKLEIN	127	127	0.000000

RESULT	9
ENTRY	
TITLE	KVMSR #type complete
	Ig kappa chain v regions (anti-arsenate hybridoma proteins) -
ORGANISM	mouse
DATE	#formal_name Mus musculus #common name house mouse
	06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change
	05-Apr-1995

**ACCESSIONS** A01927  
**REFERENCE** A01927  
**authors** Siegelman, M.; Capra, J. D.  
**#journal** Proc. Natl. Acad. Sci. U.S.A. (1981) 78:7679-7683  
**#title** Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.

```

#cross-references W01D:82150934
#accession A01927
##molecule_type protein
##residues 1-108 ##label S1E
##experimental_source strain A/J
##note hp 9367 differs in having 93-Met; HP 123E6 differs in
having 7-Ser, 92-Tyr, and 93-Met; HP 124E1 differs in
having 30-Asn, 92-Lys, and 93-Thr; and HP 91A3 differs
in having 8-Pro, 30-Asn, 37-Arg, 84-Ser, and 93-Ala
COMMENT The sequence shown is HP R16.7.

```

COMMENT The sequence shown is HP R16.7.  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 FEATURE  
 23-88 #disulfide\_bonds #status predicted  
 SUMMARY #length 108 #molecular\_weight 11910 #checksum 1537

Query Match 78.5%; Score 714; DB 2; Length 108;  
Best Local Similarity 94.4%; Pred. No. 1.80e-69;  
Matches 101; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

**Db** 1 diqmtqtssleaslgdrvtiscrasqdlsynlwyqqkpdgtvklllyytsrlhsqvps 60  
|||||  
**Qv** 21 DIQMOTSSLSASLGDRVTISCRASODISSYNWYQQKPDGTIKLLIYYTSRLHSQVPS 80  
|||||

```
Db      61 rfsgsgsgtdysltisnlegediatyfcagngslprtfgggatkleik 107
        |||||
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Ov      81 RFSGSGSGTDSYTIINLEEDIAFYFCOOGNTPIYFEGGKTFEIN 127
```

RESULT	10	
ENTRY		#type complete
	A28044	

TITLE	Ig kappa chain V region (22B5) - mouse
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	19-May-1989 #sequence revision 19-May-1989 #text change 12-Apr-1995

ACCESSIONS	A28044
REFERENCE	A94179
#authors	Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
#journal	Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248
#title	Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.

```

#cross-references MUID:87317629
#accession A28044
#molecule type mRNA

```

```

#sequence_type      1-107  ##label MEE
#residues
CLASSIFICATION      #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY              #length 107  #molecular-weight 11832  #checksum 7241

```

Query Match 78.4%; Score 713; DB 5; Length 107;  
Best Local Similarity 94.4%; Pred. No. 2.38e-69;  
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 1 di qm tqt tss lsa sl gdr vt is cras qd is n l n w y q q k p d g t v k l l i y v t s r l h s g v p s 60  
|||||  
Qv 21 d i o m t o t t s s l s a s i g n r v t i s c r a s o d i t s s y n l n w y o o k p d c t k i l l i y v t s r l h s g v p s 80  
|||||

61	rfsqsgvgtgvalinnlegediatyfcaggktlprtfgggkkleik	107
62		
63		
64		
65		
66		
67		
68		
69		
70		
71		
72		
73		
74		
75		
76		
77		
78		
79		
80		
81	rfsqsgvgtgvalinnlegediatyfcaggktnlprtfgggkkleik	127
82		
83		
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89		
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97		
98		
99		
100		

RESULT	11
ENTRY	S38862
TITLE	Iq kappa chain V region - mouse
ORGANISM	#formal_name Mus musculus #common name house mouse
DATE	06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 06-Feb-1995

ACCESSIONS  
 S38862  
 S37200  
 REFERENCE  
 #authors  
 Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.  
 #submission  
 submitted to the EMBL Data Library, August 1993  
 #description  
 production and cloning of TWV-specific monoclonal antibodies.  
 #accession  
 S38862

```

#accession      330802
##status        preliminary
##molecule_type mRNA
##residues      1-108  ##label FIS
##cross-references EMBL:X75854
SUMMARY
      #length 108  #molecular-weight 11865  #checksum 1472

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Query Match	78.0%;	Score 709;	DB 11;	Length 108;
Best Local Similarity	92.6%;	Pred. No. 7.32e-69;		
Matches 100;	Conservative 6;	Mismatches 1;	Indels 1;	Gaps 1;

**Db** 1 dvqmtqtsslaaslgdrvtiscrasqdlsynlwnyqqkpdgtvklllyvtsrlhsqvps 60  
|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||  
**Ov** 21 DIOMTOTTSSLASLGRVITICRSADISSYLNWYQKPDGTIKILYYTSRLHSQVPS 80

Accession	Gene	Protein	Length	Score	E-value
61	rfsagsgdysltienleqdiatyfcaqantlppwtfgggtk	leik	108	10.0	1.0e-22
81	rfsagsgdysltienleqdiatyfcaqantlppwtfgggtk	leik	108	10.0	1.0e-22

RESULT	12
ENTRY	PH0888 #type fragment

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9

TITLE Ig light chain V region (anti-CD3) - mouse (fragment)  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 12-Apr-1995  
 ACCESSIONS PH0888  
 REFERENCE PH0885  
 #authors Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodriguez, M.L.;  
 Beverley, P.C.L.; Feldmann, M.; Carter, P.  
 #journal J. Exp. Med. (1992) 175:217-225  
 #title Development of humanized bispecific antibodies reactive with  
 cytotoxic lymphocytes and tumor cells overexpressing the  
 HER2 protooncogene.  
 #cross-references MUID:92113462  
 #accession PH0888  
 ##molecule\_type mRNA  
 ##residues 1-109 ##label SHA  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY #length 109 #checksum 4838

Query Match 77.9%; Score 708; DB 5; Length 109;  
 Best Local Similarity 92.5%; Pred. No. 9.70e-69;  
 Matches 99; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 1 diqmtqtsslaaslgdrvtiscrasqdiynylnwyqkpdgtvkllytirlhsgvps 60  
 Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTGKLIYYTSRLHSGVPS 80

Db 61 kfsgsgtdyaltienlegediatyfcqgntlpwcfaggtkleik 107  
 Qy 81 RFSGSGGTDYSLTINNLEQEDIATYFCQGGNTLPYFGGGTKLEIN 127

RESULT 13

ENTRY S32188 #type fragment  
 TITLE Ig kappa chain V region - mouse (fragment)  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 12-Apr-1995

ACCESSIONS S32188  
 REFERENCE S32185  
 #authors Izui, S.  
 #submission submitted to the EMBL Data Library, February 1993  
 #accession S32188  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-107 ##label IZU  
 ##cross-references EMBL:X70090

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY #length 107 #checksum 7079

Query Match 77.68%; Score 705; DB 5; Length 107;  
 Best Local Similarity 91.6%; Pred. No. 2.25e-68;  
 Matches 98; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 diqmtqtsslaaslgdrvtiscrasqdiynylnwyqkpdgtvkllytirlhsgvps 60  
 Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTGKLIYYTSRLHSGVPS 80

Db 61 kfsgsgtdyaltienlegediatyfcqgntlpwcfaggtkleik 107  
 Qy 81 RFSGSGGTDYSLTINNLEQEDIATYFCQGGNTLPYFGGGTKLEIN 127

RESULT 14

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10

ENTRY PLO282 #type fragment  
 TITLE Ig light chain V region (45-49, anti p-azophenylarsonate) -  
 mouse (fragment)  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Sep-1995  
 ACCESSIONS PLO282  
 REFERENCE PLO281  
 #authors Wysocki, L.J.; Geftter, M.L.; Margolies, M.N.  
 #journal J. Exp. Med. (1990) 172:315-323  
 #title Parallel evolution of antibody variable regions by somatic  
 processes: Consecutive shared somatic alterations in VH  
 genes expressed by independently generated hybridomas  
 apparently acquired by point mutation and selection rather  
 than by gene conversion.

#accession PLO282  
 ##molecule\_type mRNA  
 ##residues 1-108 ##label WYS  
 ##experimental\_source A/J mice  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 KEYWORDS antibody; immunoglobulin  
 SUMMARY #length 108 #checksum 960

Query Match 76.7%; Score 697; DB 5; Length 108;  
 Best Local Similarity 91.6%; Pred. No. 2.12e-67;  
 Matches 98; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 diqmtqtsslaaslgdrvtiscrasqdiynylnwyqkpdgtvkllytkslsgvps 60  
 Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTGKLIYYTSRLHSGVPS 80

Db 61 kfsgsgtdyaltienlegediatyfcqgntlprtfgggtkleik 107  
 Qy 81 RFSGSGGTDYSLTINNLEQEDIATYFCQGGNTLPYFGGGTKLEIN 127

RESULT 15

ENTRY B26405 #type complete  
 TITLE Ig kappa chain V region (1F6) - mouse  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 30-Sep-1993

ACCESSIONS B26405  
 REFERENCE A90518  
 #authors Smith, J.A.; Margolies, M.N.  
 #journal Biochemistry (1987) 26:604-612  
 #title Complete amino acid sequences of the heavy and light chain  
 variable regions from two A/J mouse antigen nonbinding  
 monoclonal antibodies bearing the predominant p-azophenyl  
 arsonate idiotype.  
 #cross-references MUID:87157677

#accession B26405  
 ##molecule\_type protein  
 ##residues 1-108 ##label SMI  
 ##experimental\_source strain A/J  
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY #length 108 #molecular-weight 11985 #checksum 1541

Query Match 76.3%; Score 694; DB 5; Length 108;  
 Best Local Similarity 92.5%; Pred. No. 4.91e-67;  
 Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 1 diqmtqtsslaaslgdrvtiscrasqdiynylnwyqkpdgtvkllytkslsgvps 60  
 Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTGKLIYYTSRLHSGVPS 80

**Figure 1**

Qy 81 RFSGSGTDSLTTNNLEQEDATYFCQCGNTLPYTFGGGCKLEIN 127

Search completed: Mon Jul 8 08:32:39 1996  
Job time : 28 secs.



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W P S R L H (TW)

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WPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:31:42 1996; MacPar time 4.05 Seconds  
480.396 Million cell updates/sec

Tabular output not generated.

Title: >US-08-137-117B-29  
Description: (1-127) from US08137117B.pep  
Perfect Score: 909  
Sequence: 1 MVSSAQFLGILLICLTQGRG.....CQQNTLPYFGGKLEIN 127

Scoring table: PAM 150  
Gap 11

Searched: 43470 seqs, 15335248 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot31  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8

Statistics: Mean 41.298; Variance 69.545; scale 0.594

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description	Pred. No.
1	714	78.5	108	4	KV5K_MOUSE	IG KAPPA CHAIN V-V RE	1.57e-141
2	711	78.2	108	4	KV5L_MOUSE	IG KAPPA CHAIN V-V RE	8.46e-141
3	710	78.1	108	4	KV5N_MOUSE	IG KAPPA CHAIN V-V RE	1.48e-140
4	701	77.1	108	4	KV5M_MOUSE	IG KAPPA CHAIN V-V RE	2.30e-138
5	698	76.8	108	4	KV5O_MOUSE	IG KAPPA CHAIN V-V RE	1.24e-137
6	684	75.2	108	4	KV5U_MOUSE	IG KAPPA CHAIN V-V RE	3.14e-134
7	653	71.8	108	4	KV5J_MOUSE	IG KAPPA CHAIN V-V RE	1.04e-126
8	627	69.0	129	4	KV1W_HUMAN	IG KAPPA CHAIN PRECUR	2.04e-120
9	618	68.0	130	4	KV5G_MOUSE	IG KAPPA CHAIN PRECUR	3.05e-118
10	605	66.6	129	4	KV1X_HUMAN	IG KAPPA CHAIN PRECUR	4.17e-115
11	593	65.2	117	4	KV1I_HUMAN	IG KAPPA CHAIN PRECUR	3.24e-112
12	591	65.0	128	4	KV5E_MOUSE	IG KAPPA CHAIN PRECUR	9.82e-112
13	564	62.0	108	4	KV5P_MOUSE	IG KAPPA CHAIN V-V RE	3.01e-105

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14	564	62.0	108	4	KV1O_HUMAN	IG KAPPA CHAIN V-I RE	3.01e-105
15	561	61.7	117	4	KV1J_HUMAN	IG KAPPA CHAIN PRECUR	1.58e-104
16	559	61.5	108	4	KV1N_HUMAN	IG KAPPA CHAIN V-I RE	4.76e-104
17	553	60.8	108	4	KV1P_HUMAN	IG KAPPA CHAIN V-I RE	1.30e-102
18	543	59.7	115	4	KV5F_MOUSE	IG KAPPA CHAIN PRECUR	3.22e-100
19	542	59.6	108	4	KV1B_HUMAN	IG KAPPA CHAIN V-I RE	5.59e-99
20	538	59.2	108	4	KV1S_HUMAN	IG KAPPA CHAIN V-I RE	5.05e-99
21	536	59.0	108	4	KV1E_HUMAN	IG KAPPA CHAIN V-I RE	1.52e-98
22	529	58.2	108	4	KV1A_HUMAN	IG KAPPA CHAIN V-I RE	7.13e-97
23	529	58.2	108	4	KV1D_HUMAN	IG KAPPA CHAIN V-I RE	7.13e-97
24	527	58.0	107	4	KV1D_HUMAN	IG KAPPA CHAIN V-I RE	2.14e-96
25	527	58.0	108	4	KV1L_HUMAN	IG KAPPA CHAIN V-I RE	2.14e-96
26	524	57.6	117	4	KV5H_MOUSE	IG KAPPA CHAIN PRECUR	1.11e-95
27	508	55.9	108	4	KV1R_HUMAN	IG KAPPA CHAIN V-I RE	7.19e-92
28	507	55.8	108	4	KV1M_HUMAN	IG KAPPA CHAIN V-I RE	1.24e-91
29	507	55.8	109	4	KV1T_HUMAN	IG KAPPA CHAIN V-I RE	1.24e-91
30	506	55.7	108	4	KV5S_MOUSE	IG KAPPA CHAIN V-V RE	2.15e-91
31	505	55.6	108	4	KV1C_HUMAN	IG KAPPA CHAIN V-I RE	3.71e-91
32	505	55.6	136	4	KV5B_MOUSE	IG KAPPA CHAIN PRECUR	3.71e-91
33	504	55.4	108	4	KV5Q_MOUSE	IG KAPPA CHAIN V-V RE	6.42e-91
34	503	55.3	108	4	KV1V_HUMAN	IG KAPPA CHAIN V-I RE	1.11e-90
35	503	55.3	108	4	KV1Q_HUMAN	IG KAPPA CHAIN V-I RE	1.11e-90
36	500	55.0	108	4	KV5T_MOUSE	IG KAPPA CHAIN V-V RE	5.73e-90
37	500	55.0	115	4	KV5C_MOUSE	IG KAPPA CHAIN PRECUR	5.73e-90
38	496	54.6	108	4	KV1G_HUMAN	IG KAPPA CHAIN V-I RE	5.10e-89
39	495	54.5	108	4	KV1K_HUMAN	IG KAPPA CHAIN V-I RE	8.81e-89
40	495	54.5	129	4	KV3L_HUMAN	IG KAPPA CHAIN PRECUR	8.81e-89
41	493	54.2	129	4	KV3M_HUMAN	IG KAPPA CHAIN PRECUR	2.63e-88
42	491	54.0	108	4	KV5D_MOUSE	IG KAPPA CHAIN V-V RE	7.84e-88
43	491	54.0	108	4	KV1F_HUMAN	IG KAPPA CHAIN V-I RE	7.84e-88
44	490	53.9	108	4	KV5R_MOUSE	IG KAPPA CHAIN V-V RE	1.35e-87
45	489	53.8	132	4	KV3F_MOUSE	IG KAPPA CHAIN PRECUR	2.34e-87

ALIGNMENTS

RESULT	1	ID	KV5K_MOUSE	STANDARD;	PRT;	108 AA.
AC	P01644;	21-JUL-1986	(REL. 01, CREATED)			
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)				
DT	01-OCT-1993	(REL. 27, LAST ANNOTATION UPDATE)				
DE	IG KAPPA CHAIN V-V REGION (HP R16.7).					
OS	MUS MUSCULUS (MOUSE).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; RODENTIA.					
RN	[1]					
RP	SEQUENCE.					
RC	STRAIN=A/J;					
RM	82150934					
RA	SIEGELMAN M., CAPRA J.D.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).					
CC	-I- ANTI-ARSONATE HYBRIDOMA PROTEIN.					
DR	P1R; A01927; KWSAR.					
DR	HSP; P01607; IFAI.					
KW	IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.					
FT	DOMAIN 1	23	FRAMEWORK 1.			
FT	DOMAIN 2	34	COMPLEMENTARITY-DETERMINING 1.			
FT	DOMAIN 3	49	FRAMEWORK 2.			
FT	DOMAIN 4	56	COMPLEMENTARITY-DETERMINING 2.			
FT	DOMAIN 5	88	FRAMEWORK 3.			
FT	DOMAIN 6	97	COMPLEMENTARITY-DETERMINING 3.			
FT	DOMAIN 7	108	FRAMEWORK 4.			
FT	DISULFID	23	BY SIMILARITY.			

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FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; 63325 CN;

Query Match 78.5%; Score 714; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 1.57e-141;
Matches 101; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaaslgdrvtiscrasqdiennlwnyqkpdgtvkliiytsrlhsgvps 60
    |||||
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLIYYTSRLHSGVPS 80
    |||||

Db 61 rfsgsgsgtdysltisnleqediattyfcqggnmlprtfgggtkleik 107
    |||||
Qy 81 RFSGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEIN 127
    |||||

RESULT 2
ID KV5L MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP 93G7).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RM 82150934
RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KWSAR.
DR HSSP; P01607; IFAL.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 63046 CN;

Query Match 78.2%; Score 711; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 8.46e-141;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaaslgdrvtiscrasqdiennlwnyqkpdgtvkliiytsrlhsgvps 60
    |||||
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLIYYTSRLHSGVPS 80
    |||||

Db 61 rfsgsgsgtdysltisnleqediattyfcqggnmlprtfgggtkleik 107
    |||||
Qy 81 RFSGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEIN 127
    |||||

RESULT 3
ID KV5N MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (REL. 01, CREATED)

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DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP 124E1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RM 82150934
RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KWSAR.
DR HSSP; P01607; IFAL.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 63856 CN;

Query Match 78.1%; Score 710; DB 4; Length 108;
Best Local Similarity 93.5%; Pred. No. 1.48e-140;
Matches 100; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaaslgdrvtiscrasqdiennlwnyqkpdgtvkliiytsrlhsgvps 60
    |||||
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLIYYTSRLHSGVPS 80
    |||||

Db 61 rfsgsgsgtdysltisnleqediattyfcqggtklprtfgggtkleik 107
    |||||
Qy 81 RFSGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEIN 127
    |||||

RESULT 4
ID KV5M MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP 123E6).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RM 82150934
RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KWSAR.
DR HSSP; P01607; IFAL.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.

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FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 108 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11989 MW; 64511 CN;

Query Match 77.1%; Score 701; DB 4; Length 108;  
 Best Local Similarity 92.5%; Pred. No. 2.30e-138;  
 Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaealgrvrtiscrasdiynlwyqkpdgtvkllytyterlhsgvps 60  
 Qy 21 DIQMTQTSSLSASLGRVRTISCRASQDISSYLNWYQKPDGTIKLIIYTSRLHSGVPS 80  
 Db 61 rfsgsgtdyaltisnleqediatyfcqggymprtfgggkklxik 107  
 Qy 81 RFSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEIN 127

RESULT 5  
 ID KV50 MOUSE STANDARD; PRT; 108 AA.  
 AC P01648;

DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (HP 91A3).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]

RP SEQUENCE.  
 RC STRAIN=A/J;  
 RM 82150934  
 RA SIEGELMAN M., CAPRA J.D.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).  
 CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.  
 DR PIR; A01927; KMSAR.  
 DR HSSP; P01607; IFAI.  
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.

FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 108 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11961 MW; 62636 CN;

Query Match 76.8%; Score 698; DB 4; Length 108;  
 Best Local Similarity 90.7%; Pred. No. 1.24e-137;  
 Matches 91; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaealgrvrtiscrasdiynlwyqkpdgtvkllytyterlhsgvps 60  
 Qy 21 DIQMTQTSSLSASLGRVRTISCRASQDISSYLNWYQKPDGTIKLIIYTSRLHSGVPS 80  
 Db 61 rfsgsgtdyaltisnleqediatyfcqggymprtfgggkklxik 107  
 Qy 81 RFSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEIN 127

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6

RESULT 6  
 ID KV50 MOUSE STANDARD; PRT; 108 AA.  
 AC P04946;  
 DT 13-AUG-1987 (REL. 05, CREATED)  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (N05-89.4).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RM 83271467  
 RA KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;  
 RL NATURE 304:320-324(1983).  
 CC -I- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.  
 DR EMBL; K00745; WMICKAAO.  
 DR HSSP; P01607; IFAI.  
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107 FRAMEWORK 4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11866 MW; 68556 CN;

Query Match 75.2%; Score 684; DB 4; Length 108;  
 Best Local Similarity 88.8%; Pred. No. 3.14e-134;  
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaealgrvrtiscrasdiynlwyqkpdgtvkllytyterlhsgvps 60  
 Qy 21 DIQMTQTSSLSASLGRVRTISCRASQDISSYLNWYQKPDGTIKLIIYTSRLHSGVPS 80  
 Db 61 rfsgsgtdyaltisnleqediatyfcqggymprtfgggkklxik 107  
 Qy 81 RFSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEIN 127

RESULT 7  
 ID KV50 MOUSE STANDARD; PRT; 108 AA.  
 AC P01643;

DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-V REGION (MOPC 173).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]

RP SEQUENCE.  
 RM 76091934  
 RA SCHIFF C., FOUCEREAU M.;  
 RL EUR. J. BIOCHEM. 59:525-537(1975).  
 CC -I- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR; A01926; KMS73.  
 DR HSSP; P01607; IFAI.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.

FT	DOMAIN	35	49	FRAMEWORK 2.
FT	DOMAIN	50	56	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	57	88	FRAMEWORK 3.
FT	DOMAIN	89	97	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	98	108	FRAMEWORK 4.
FT	DISULFID	23	88	BY SIMILARITY.
FT	NON TER	108	108	
SQ	SEQUENCE	108 AA;	111819 MW;	73271 CN;

Query Match	71.8%;	Score 653;	DB 4;	Length 108;
Best Local Similarity	82.2%;	Pred. No. 1.04e-126;		
Matches	88;	Conservative	12;	Mismatches 7; Indels 0; Gaps 0;
Db	1	digmqttsleaelgdvrtiescasasignylbwqqkpdgtvklllytsslhsgvps	60	
Qy	21	dIQMTQTSSLSALGRVTVTISCRASQDISSYLNWYQKQPDGTKILLIYVTSRLHSGVPS	80	
Db	61	rfgsgsgtdysltisblzpbziatyccqycklprffgggtkleik	107	
Qy	81	RFGSGSGTDYSLTINNLLEDQDIATYFCOQNTLPYFVGGETKLEIN	127	

RESULT	8
ID	KV1W HUMAN STANDARD; PRT; 129 AA.
AC	P04431;
DT	13-AUG-1987 (REL. 05, CREATED)
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN PRECURSOR V-I REGION (WALKER).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
[1]	
RN	SEQUENCE FROM N.A.
RM	85014148
RA	KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
RL	NUCLEIC ACIDS RES. 12:6995-7006(1984).
DR	EMBL; X00965; HSVK01.
DR	PIR; A01883; K1HUWK.
DR	HSSP; P01607; 2FCW.
KW	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL 1 22
FT	CHAIN 23 129 IG KAPPA CHAIN V-I REGION (WALKER).
FT	DOMAIN 23 45 FRAMEWORK 1.
FT	DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 57 71 FRAMEWORK 2.
FT	DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 79 110 FRAMEWORK 3.
FT	DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN 120 129 FRAMEWORK 4.
FT	DISULFID 45 110 BY SIMILARITY.
FT	NON TER 129 129
SQ	SEQUENCE 129 AA; 14069 MW; 94965 CN;

```
Query Match      69.0%; Score 627; DB 4; Length 129;
Best Local Similarity 68.5%; Pred. No. 2,046-120;
Matches 87; Conservative 22; Mismatches 18; Indels 0; Gaps 0

Db       3   mrvpagllglllwlrgardcmtqspsslsasvqdrvtitrcasgsenylnwqkqp 62
          | :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy       1   MYSSAQLGALLLFCQCTRCIDQMGTTSLSASLGDRVITISCRASQDISYLLNYYQQKP 60

Db       63  gkapklllyaaaslsgsvtfrfsgsgsdftltisslpqedaatyvcqsystltffg 122
          : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
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Qy	61	DTIKLLIYYTSRLHSGVPSFGSGSGD <sup>1</sup> SLTINNLEQED <sup>1</sup> ATYFCQCGNTLP <sup>1</sup> YFEGG <sup>1</sup> 120
Db	123	qtrleik <sup>1</sup> 129
		: : :
Qy	121	GTKLEIN <sup>1</sup> 127

RESULT	9	
ID	KV5G MOUSE	STANDARD; PRT; 130 AA.
AC	P01639; P01640;	
DT	21-JUL-1986 (REL. 01, CREATED)	
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)	
DE	IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).	
OS	MUS MUSCULUS (MOUSE).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; RODENTIA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RM	79221900	
RA	SEIDMAN J.G., MAX E.E., LEDER P.;	
RL	NATURE 280:370-375 (1979).	
RN	[2]	
RP	SEQUENCE OF 1-33.	
RM	71148916	
RA	BURSTEIN Y., SCHECHTER I.;	
RL	PROC. NATL. ACAD. SCI. U.S.A. 74:716-720 (1977).	
RN	[3]	
RP	SEQUENCE OF 23-130.	
RM	67056897	
RA	GRAY W.R., DREYER W.J., HOOD L.;	
RL	SCIENCE 155:465-467 (1967).	
CC	-!- THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY	
CC	MNA ISOLATED FROM MYELOMA POLYSOMES.	
CC	-!- THIS IS A BENCE-JONES PROTEIN.	
CC	PIR; A01922; KVM5M4.	
DR	HSP; P01607; 6FAB.	
KW	IMMUNOGLOBULIN V REGION; SIGNAL; BENCE-JONES PROTEIN.	
FT	SIGNAL 1 22	
FT	CHAIN 23 116	IG KAPPA CHAIN V-V REGION (MOPC 41).
FT	DOMAIN 23 45	FRAMEWORK 1.
FT	DOMAIN 46 56	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 57 71	FRAMEWORK 2.
FT	DOMAIN 72 78	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 79 110	FRAMEWORK 3.
FT	DOMAIN 111 119	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN 120 129	FRAMEWORK 4.
FT	VARIANT 1 2	MISSING (IN 25% OF THE MOLECULES).
FT	DISULFID 45 110	BY SIMILARITY.
FT	NON TER 130 130	
SQ	SEQUENCE 130 AA; 14311 MW; 96159 CN;	

	Query Match	Best Local Similarity	Score 618;	DB 4;	Length 130;
	Matches	89;	Conservative	18;	Mismatches 20;
				Indels	0;
				Gaps	0;
Db	3	mrpaqifglllllfggtrcdtqmtqpssalslqervaltcrasqdgslnwlqep	62		
		: : :   :                         : : :			
Oy	1	MVSSAOFGLGILLLCFOQTRCDIQMTQTSSLSASLGDRVTISCRASQDISYLNWYQOKP	60		
Db	63	dgtkrllyatesldsgvpkrfsgsregdyaltislaesefdvyclqvaspwtfgg	122		
Ov	61	DCTIKLIIYVTSRLHSCWPSRFSSGSGCTDYSLTNLNEEDIATFYCOOGNTLPYTFGG	120		

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Db 123 gtleik 129
      |||||:
Qy 121 gtlein 127

RESULT 10
ID KV1X HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-I REGION (DAUDI).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE FROM N.A.
RM 85014148
RA KLOBECK H.G.; COMBIATO G.; ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 12:6995-7006(1984).
DR ENBL; X00966; HSWK02.
DR PIR; A01884; KIHUDI.
DR HSSP; P01607; 1FGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 22
FT FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION (DAUDI)
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 120 129 FRAMEWORK 4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; 93457 CN;

Query Match 66.6%; Score 605; DB 4; Length 129;
Best Local Similarity 61.6%; Pred. No. 4.17e-115;
Matches 77; Conservative 30; Mismatches 18; Indels 0;

Db 3 mrvpqllgllllwlrivrddiqmtqgsalsasvgrvrtictaghnitnflwysv
Qy 1 MVSNAQFGLGILLLCFGCTGCDIQMTQTSSLSASLGDRVTTISCRASQDISSVILWYQV
Db 63 gkaptllliavsnlqvqvpvrfsgsgaeftllisslqpedfatvycqmqvnfsftf
Qy 61 DETIKLLIYTRLLHSGVPSRSGSGSDYSLTINNLSQEDDIATYFCQQGNTPYPT
Db 123 gtkvd 127
      |||||:
Qy 121 gtleik 125

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RESULT	11
ID	KVII HUMAN STANDARD; PRT; 117 AA.
AC	P01601;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN PRECURSOR V-I REGION (HK101) (FRAGMENT).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.

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RN [1]
RP SEQUENCE FROM N.A.
RM 81098966
RA BENTLEY D.L., RABBITTS T.H.;
RL NATURE 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RM 83129397
RA BENTLEY D.L., RABBITTS T.H.;
RL CELL 32:181-189(1983).
DR EMBL; V00558; HSI6K2.
DR PIR; A01881; KIH011.
DR HSP; A21056; A21056.
DR HSP; P01607; IDFB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION (HK101).
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12799 MW; 78561 CN;

Query Match 65.2%; Score 593; DB 4; Length 117;
Best Local Similarity 72.1%; Pred. No. 3,24e-112;
Matches 80; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

Db 7 aqlgllllcpgardcmtqspsslsasvqdrvtitcrarqgisslwlawyqgkpek 66
||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
QY 5 AQFLGULLLCFGTRCDQMTQTSSLSASLGDRVITCRASQDISSYLAWYQQRPDGTI 64
||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
Db 67 kslivaasslsgvparfagsqtdftlisslqpedfatyycqynsyp 117
| || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 65 KLLIYTSRLHSGVPSRFGSGSGCTDYSLTINNLEQEDATYFCQCGNTLP 115

RESULT 12
ID KV5E MOUSE STANDARD; PRT; 128 AA.
AC P01637;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-V REGION (T1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [11]
RP SEQUENCE FROM N.A.
RM 81052342
RA ALTENBURGER W., STEINMETZ M., ZACHAU H.G.;
RL NATURE 287:603-607(1980).
DR PIR; A01920; KVMST1.
DR HSP; P01607; I1IF.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION (T1).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.

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	FT	DMAIN	77	108	FRAMEWK 3.
	FT	DMAIN	109	117	COMPLEMENTARITY--DETERMINING 3.
	FT	DMAIN	118	127	FRAMEWK 4.
	FT	DISULFID	43	108	BY SIMILARITY.
	FT	NON TER	128	128	
	SQ	SEQUENCE	128 AA;	14385 MW; 91208 CN;	
		Query Match		65.0%;	Score 591; DB 4; Length 128;
		Best Local Similarity		63.0%;	Pred. No. 9.82e-112;
		Matches	80;	Conservative	25; Mismatches 22; Indels 0; Gaps
Db	1	mrtpeqfllgilllwfpgikcdiktmspsmyaelgservtiectasqdinsyltfvqqkp	60		
	:	: ::  ::     :    :: :	:	:	:
QY	1	MVSSAQFLGILLLCFOGTQRCDIQMTOTTSLSASIGDRVTISCRASQDISSYLNNYYQQKP	60		
	:	: ::  ::     :    :: :	:	:	:
Db	61	gkspktlylrantlvdgvprsfsgsqgdskfaltissleyedmgtyvcldydefplftga	120		
	:	: ::  ::     :    :: :	:	:	:
QY	61	DTGIKLLIYTSLRHLHSGVPFRFSGSCTDYSLTINNLEGEDIAITFCQGQTLPFYFGG	120		
	:	: ::  ::     :    :: :	:	:	:
Db	121	gtklelk	127		
	:	: ::  ::     :    :: :	:	:	:
QY	121	GTKLEIN	127		

RESULT	13
ID	KVSP MOUSE STANDARD; PRT; 108 AA.
AC	P01649;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN V-V REGIONS (ANTI-ARSONATE ANTIBODIES).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
QC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE.
RC	STRAIN=A/J;
RM	71250895
RA	CAPRA J.D., TUNG A.S., NISONOFF A.;
RL	J. IMMUNOL. 119:993-999(1977).
CC	-!- THE MIXTURE SEQUENCED CONTAINED AT LEAST TWO OR THREE DIFFERENT LIGHT CHAINS. PEPTIDES CONTAINING THE FOLLOWING SUBSTITUTIONS WERE ALSO ISOLATED: 3-VAL, 10-ILE, AND 12-LEU; 22-LEU; 36-PHE, 41-GLU, AND 43-ALA; 63-THR AND 68-ARG; 76-SER, 77-SER, 78-VAL, 80-ALA, AND 85-ASP; AND 100-GLN AND 107-ARG.
CC	PIR; A01928; KWSAA.
DR	HSSP; P01607; IFAI.
KW	IMMUGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT	DOMAIN 1 23 FRAMEWORK 1.
FT	DOMAIN 24 34 COMPLEMENTARITY--DETERMINING 1.
FT	DOMAIN 35 49 FRAMEWORK 2.
FT	DOMAIN 50 56 COMPLEMENTARITY--DETERMINING 2.
FT	DOMAIN 57 88 FRAMEWORK 3.
FT	DOMAIN 89 97 COMPLEMENTARITY--DETERMINING 3.
FT	DOMAIN 98 108 FRAMEWORK 4.
FT	DISULFID 23 88 BY SIMILARITY.
FT	NON TER 108 108
SQ	SEQUENCE 108 AA; 12056 MW; 62234 CN;

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Query Match      62.0%; Score 564; DB 4; Length 108;
Best Local Similarity 73.8%; Pred.No. 3.01e-105;
Matches 79; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
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Db 1 diqmtatpsslsaslgdrvsiscrasqdlsqwlfwyqackpqgppklliyrvsrItngvpd 60

Qy	21	DIQMTOTSSLSGLDRVTISCRASODISSYINWYQKPDGTKILLIYYTSRLHGSVP	80
Db	61	rfgsgsgtdftlidpmeeddatyfcqqsrliprtfgggtkleik	107
Qy	81	RFGSGSGSDYTLNNLGGEDIATYFCQCGNTYTFYFGGKTLEIN	127

RESULT	14
ID	KVIO HUMAN STANDARD; PRT; 108 AA.
AC	P01607;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, SEQUENCE UPDATE)
DT	01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN V-I REGION (REI).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE.
RM	76023758
RA	PALM W., HILSCHMANN N.;
RL	HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:167-191(1975).
RN	[2]
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RM	76039968
RA	EPP O., LATTMAN E.E., SCHIFFER M., HUBER R., PALM W.;
RL	BIOCHEMISTRY 14:4943-4952(1975).
CC	-!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC	-!- THIS IS A BENCE-JONES PROTEIN.
DR	PIB; A01873; KIURE.
DR	PDB; IREI; 17-FEB-84.
KW	IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE.
FT	DOMAIN 1 23 FRAMEWORK 1.
FT	DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 35 49 FRAMEWORK 2.
FT	DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 57 88 FRAMEWORK 3.
FT	DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN 98 107 FRAMEWORK 4.

Query Match 62.0%; Score 564; DB 4; Length 108;

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Best Local Similarity 72.6%; Pred. No. 3.01e-105;  
Matches 77; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

Db 1 dmqmtqpsleasvgrvtitcasqdiikynwygqtpgkapklllyeaaqlcagvps 60

Qy 21 DIQMTQTSSLSASLGRVITISCRASQDISSYINWYQQRPDGTIKLLIYYTSLRLHSGVPS 80

Db 61 rfsqsgsgtdyftislqpediatyccqyqslpytfgggtklqi 106

Qy 81 RESGSGTDSLTLNNLEQEDIATYFCQGGNTLPYTFGGGTKEI 126

RESULT 15

ID KVLJ HUMAN STANDARD; PRT; 117 AA.

AC P01602;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN PRECURSOR V-I REGION (HK102) (FRAGMENT) .

OS HOMO SAPIENS (HUMAN) .

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RM 81098966

RA BENTLEY D.L., RABBITTS T.H.;

RL NATURE 288:730-733(1980) .

DR EMBL; Z00001; H5IGK3.

DR PIR; A01882; KIHU12.

DR HSSP; P01607; 1DFB.

KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT SIGNAL 1 22

FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION (HK102) .

FT DOMAIN 23 45 FRAMEWORK 1.

FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 57 71 FRAMEWORK 2.

FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 79 110 FRAMEWORK 3.

FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING 3.

FT DISULFID 45 110 BY SIMILARITY.

FT NON\_TER 117 117

SQ SEQUENCE 117 AA; 12768 MW; 80156 CN;

Query Match

Best Local Similarity 61.7%; Score 561; DB 4; Length 117;

Matches 75; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

Db 3 mrvpaqlgllllwlpgakcdiqmtcqpstleasvgrvtitcrasqiswlawyqkxp 62

Qy 1 MWSAQLGLLLLCFQCTRCDTQMTQTSSLSASLGRVITISCRASQDISSYINWYQQR 60

Db 63 gkapklliydasslesgvpfsqsgstftltisslpddfatvycqq 112

Qy 61 DGTIKLLIYYTSLRLHSGVPSRFSGSGTDSLTLNNLEQEDIATYFCQ 110

Search completed: Mon Jul 8 08:31:55 1996

Job time : 13 secs.



(ML)

I L K N Q X

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:32:56 1996; MasPar time 4.21 Seconds  
250.053 Million cell updates/sec

Tabular output not generated.

Title: >US-08-137-117B-29

Description: (1-127) from US08137117B.ppt

Perfect Score: 909  
Sequence: 1 MVSSAQFLGLLLLCFQGR.....CQQGNTLPYFGGGKLEIN 127

Scoring table: PAM 150  
Gap 11

Searched: 70887 seqs, 8282111 residues

Post-processing: Minimum Match 0%  
Listing first 45

Database: a-geneseq22  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14

Statistics: Mean 30.127; Variance 164.919; scale 0.183

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	909	100.0	127	6	R28670	pPM-k3 protein produc	1.06e-59
2	879	96.7	131	14	R84553	Mab SCH94.03 light ch	2.18e-57
3	876	96.4	127	6	R32121	Anti-CD4 antibody MT	3.72e-57
4	860	94.6	128	5	R09426	ME4 Light Chain V Reg	6.37e-56
5	853	93.8	127	8	R39265	Mouse C4G1 Ig light-c	2.20e-55
6	826	90.9	127	6	R29010	p146-k3 protein produ	2.65e-53
7	818	90.0	127	2	R12359	Light (kappa) chain v	1.09e-52
8	817	89.9	126	2	R12337	Mouse Mab 1C11 L chai	1.30e-52
9	814	89.5	124	9	R47206	Human/murine IL-1 chi	2.22e-52
10	802	88.2	128	7	R33257	Rat Immunoglobulin L	1.86e-51
11	786	86.5	128	10	R53340	KM41 H chain variabl	3.16e-50
12	708	77.9	107	6	R30768	Murine anti-CD3 Mab U	3.06e-44

## ALIGNMENTS

RESULT	1	
ID	R28670 standard; Protein; 127 AA.	
AC	R28670;	
DT	30-MAR-1993 (first entry)	
DE	pM-K3 protein product.	
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;	
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;	
KW	plasmid; pM-K3; pM-hl.	
OS	Synthetic.	
EH	Key	Location/Qualifiers
FT	Peptide	1..20
FT	/note= "Signal peptide"	
FT	Protein	21..127
FT	/note= "Mature peptide"	
PN	W09219759-A.	
PD	12-NOV-1992.	
PF	24-APR-1992; J00544.	
PR	25-APR-1991; J0-095476.	
PR	19-FEB-1992; J0-032084.	
PA	(CHUS ) CHUGAI SEIYAKU KK.	
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;	
DR	WPI; 92-398882/48.	
DR	N-PSDB; Q30755.	
PT	Reconstituted human antibody to human interleukin-6 receptor -	
PT	has low antigenicity and contains mouse V-region complementarity	
PT	determining regions	
PS	Disclosure; Page 121-122; 207pp; Japanese.	

CC The sequences given in R28670-71 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PM1 which contained the plasmids pPM-k3 and pPM-h1.

CC Sequence 127 AA;

Query Match 100.0%; Score 909; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 1.06e-59;  
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mvssaqlgllllcfqgtrcdiqmtqtaslaaslgdrvtiscraasqdiaylnwyqkq 60

Qy 1 WVSSAQFLGLLLCFQGTCTCDIQMTQTTSLSASLGDRVTISCRASQDISSYLNWYQKQ 60

Db 61 dgtikllyvtterlshgvsprfsgsgtdyaltinnleqediatyfcqgntlpvtfgg 120

Qy 61 DGTIKLLIYVTSRLHSGVSPRFSGSGTDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120

Db 121 gtklein 127

Qy 121 GTKLEIN 127

#### RESULT 2

ID R84553 standard; Protein; 131 AA.

AC R84553;

DT 02-FEB-1996 (first entry)

DE MAb SCH94.03 light chain.

KW Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system;

KW CNS; demyelination; multiple sclerosis; neural disease; therapeutic.

OS Mus sp.

FH Key Location/Qualifiers

FT Peptide 1..20

FT /Label= Leader\_peptide

FT Region 44..54

FT /Label= CDR1

FT Region 70..76

FT /Label= CDR2

FT Region 109..117

FT /Label= CDR3

FT Region 116..128

FT /Label= Joining\_region

FT Region 129..131

FT /Label= C-kappa\_region

PN W09530004-A1.

PD 09-NOV-1995.

PF 27-APR-1995; U05262.

PR 29-APR-1994; US-236520.

PA (MAYO-) MAYO FOUNDATION.

PI Miller DJ, Rodriguez M;

DR WPI; 95-393077/50.

DR N-PSDB; T05311.

PT Monoclonal antibodies which stimulate central nervous system

PT re-myelination - are produced by hybridoma ATCC CRL 11627, for

PT treating multiple sclerosis, and viral or post-neural diseases of

PT the CNS.

PS Disclosure; Page 36-37; 63pp; English.

CC Hybridoma ATCC CRL 11627 was obtained from a SJL/J mouse injected with

CC spinal cord homogenate from a mammal uninfected with any

CC demyelinating disease. The hybridoma produced a monoclonal antibody

CC (SCH94.03) useful in promoting CNS remyelination. The SCH94.03

CC light chain amino acid sequence is given in R84553.

SQ Sequence 131 AA;

Query Match 96.7%; Score 879; DB 14; Length 131;  
Best Local Similarity 95.3%; Pred. No. 2.18e-57;  
Matches 121; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mmssaqlgllllcfqgtrcdiqmtqtaslaaslgdrvtiscraasqdiaylnwyqkq 60

Qy 1 WVSSAQFLGLLLCFQGTCTCDIQMTQTTSLSASLGDRVTISCRASQDISSYLNWYQKQ 60

Db 61 dgtvkllyvtterlshgvsprfsgsgtdyaltinnleqediatyfcqgntlpvtfgg 120

Qy 61 DGTIKLLIYVTSRLHSGVSPRFSGSGTDYSLTINNLEQEDIATYFCQGNLTLPYTFGG 120

Db 121 gtleik 127

Qy 121 GTKLEIN 127

#### RESULT 3

ID R32121 standard; Protein; 127 AA.

AC R32121;

DT 02-JUN-1993 (first entry)

DE Anti-CD4 antibody MT 15.1 light chain variable region.

KW immunosuppression; tissue transplantation; graft; L chain; V region;

KW T-helper cell inhibition; transplant rejection; MAb;

KW interleukin-2 receptor.

FH Key Location/Qualifiers

FT Peptide 1..20

FT /Label= signal

FT Region 21..115

FT /Label= Variable

FT Region 116..127

FT /Label= J2

PN DE4143214-A.

PD 28-JAN-1993.

PF 30-DEC-1991; 143214.

PR 25-JUL-1991; DE-124759.

PR 30-DEC-1991; DE-143214.

PA (BOEY) BOEHRINGER MANNHEIM GMBH.

PI Kaluza B, Rietmueller G, Scheuer W, Weidle U;

DR WPI; 93-037582/05.

DR N-PSDB; Q36607.

PT Synergistic antibody compen. for use as immunosuppressant -

PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R

PT alpha- or anti-IL2R beta antibodies

PS Claim 5; Page 9; 18pp; German.

CC This sequence is the light chain variable region of a preferred

CC anti-CD4 monoclonal antibody for use in the claimed synergistic

CC composition. MAb MT 15.1 is deposited as clone 15-1/P3/14 (ECACC

CC 90090705). The anti-CD4 antibody is used with at least one anti-IL2R

CC alpha or beta antibody. Individually the antibodies are strongly

CC inhibiting and when used together their immunosuppressive properties

CC are improved; they synergistically inhibit T-helper cell

CC proliferation to effectively inhibit transplant rejection at low

CC doses without significantly reducing the general immune response.

CC See also Q36608-Q36616.

SQ Sequence 127 AA;

Query Match 96.4%; Score 876; DB 6; Length 127;

Best Local Similarity 92.9%; Pred. No. 3.72e-57;

Matches 118; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 mmssaqlgllllcfqgtrcdiqmtqtaslaaslgdrvtiscraasqdiaylnwyqkq 60

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Qy 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRTVITSCRASQDISSYLNWYQKP 60
Db 61 dqtvkliiyterlshgvsrfsqsgtdysltitnleqdvatyfcqgntlpwtfqg 120
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQGGNTLPYTFGG 120
Db 121 gtleik 127
Qy 121 GTKLEIN 127

RESULT 4
ID R09426 standard; Protein; 128 AA.
AC R09426;
DT 04-MAR-1993 (first entry)
DE ME4 Light Chain V region (mouse).
KW Monoclonal antibody; chimera; light; heavy; chain; constant;
KW variable; antigen; diagnosis; cancer; tumour.
OS Mus musculus.
PN W09002569-A.
PD 22-MAR-1990.
PF 06-SEP-1989; U03852.
PR 06-SEP-1988; US-240624.
PR 08-SEP-1988; US-241744.
PR 13-SEP-1988; US-243739.
PR 04-OCT-1988; US-253002.
PR 19-JUN-1989; US-367641.
PR 21-JUL-1989; US-382768.
PA (ITGE-) INT GENETIC ENG INC.
PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
DR WPI; 90-115825/15.
DR N-PSDB; Q08608.
PT Chimeric mouse-human antibodies - prepd. using genes coding for
PT constant human region murine variable region, esp. to 3 tumour
PT antigen
PS Claim 13; Page 123 + Fig 29; 173pp; English.
CC The sequence is used in the prodn. of a chimeric antibody mol.
CC comprising two light chains and two heavy chains, each having a
CC constant region (human) and a variable region (murine) having
CC specificity to an antigen bound by murine monoclonal antibody
CC (MAB) ME4. The chimeric antibodies can be used for any purpose for
CC which the original murine MABs can be used, with the advantage that
CC they are more compatible with the human body. They are esp. used for
CC the diagnosis and treatment of cancer.
SQ Sequence 128 AA;

Query Match 94.6%; Score 860; DB 5; Length 128;
Best Local Similarity 92.9%; Pred. No. 6.37e-56;
Matches 118; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 mmsaqlgllllcfcggtcdiqmtqtsslsaslgdrvtiscrasqdiyylnwyqkp 60
Qy 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRTVITSCRASQDISSYLNWYQKP 60
Db 61 dqtvkliiyterlshgvsrfsqsgtdysltitnleqdvatyfcqgntlpwtfqg 120
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQGGNTLPYTFGG 120
Db 121 gtleik 127
Qy 121 GTKLEIN 127
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RESULT 5
ID R39265 standard; Protein; 127 AA.
AC R39265;
DT 29-NOV-1993 (first entry)
DE Mouse C4G1 Ig light-chain.
KW Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIa/IIb;
KW monoclonal antibody; platelet agglutination; humanised antibody.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= signal_peptide
FT Protein 22..127
FT /label= light_chain
FT Region 44..54
FT /label= complementarity_determining_region_1
FT Region 70..76
FT /label= CDR 2
FT Region 109..117
FT /label= CDR 3
PN W09313133-A.
PD 08-JUL-1993.
PF 15-DEC-1992; J01630.
PR 20-DEC-1991; US-812111.
PR 09-JUN-1992; US-895932.
PR 11-SEP-1992; US-944159.
PA (PROT-) PROTEIN DESIGN LABS INC.
PA (YAMA ) YAMANOUCHI PHARM CO LTD.
PI Co MS, Tso JY;
DR WPI; 93-227275/28.
DR N-PSDB; Q45662.
PT Compns. contg. immunoglobulin specific for the GP-IIb and -IIIa
PT protein - for treating disorders related to vascular thrombosis
PS Disclosure; Fig 2A; 54pp; Japanese.
CC This is the sequence of the mouse C4G1 immunoglobulin light
CC chain. See R39266 for the heavy chain sequence. The antibody is
CC specific for the GPIIa/IIb protein and inhibits platelet
CC agglutination. The Ig is thus useful in the treatment of
CC thrombosis.
SQ Sequence 127 AA;

Query Match 93.8%; Score 853; DB 8; Length 127;
Best Local Similarity 92.1%; Pred. No. 2.20e-55;
Matches 117; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 1 mmsaqlgllllcfcggtcdiqmtqtsslsaslgdrvtiscrasqdiymlynyqkp 60
Qy 1 MVSSAQFLGILLLCFQGTCDIQMTQTSSLSASLGDRTVITSCRASQDISSYLNWYQKP 60
Db 61 dqtvkliiyterlshgvsrfsqsgtdysltitnleqdvatyfcqgntlpwtfqg 120
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQGGNTLPYTFGG 120
Db 121 gtleik 127
Qy 121 GTKLEIN 127

RESULT 6
ID R29010 standard; Protein; 127 AA.
AC R29010;
DT 30-MAR-1993 (first entry)
DE pl46-k3 protein product.
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;
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KW plasmid; p146-k3; p146-h1.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /note= "Signal peptide"  
 FT Protein 21..127  
 FT /note= "Mature peptide"  
 PN W09219759-A.  
 PD 12-NOV-1992.  
 PF 24-APR-1992; J00544.  
 PR 25-APR-1991; JP-095476.  
 PR 19-FEB-1992; JP-032084.  
 PA (CHUS) CHUGAI SEIYAKU KK.  
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 DR WPI; 92-398882/48.  
 DR N-PSDB; Q30759.  
 PT Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 PS Disclosure; Page 127-128; 207pp; Japanese.  
 CC The sequences given in R29010-11 were encoded by plasmids which were  
 CC used in example to illustrate the production of a human antibody which  
 CC recognises human interleukin-6 receptor (IL-6R). The antibody  
 CC comprises light (L) chain and heavy (H) chain variable regions which  
 CC were derived from a mouse monoclonal antibody produced from the  
 CC hybridoma AUK146-15 which contained the plasmids p146-k3 and p146-h1.  
 SQ Sequence 127 AA;

Query Match 90.9%; Score 826; DB 6; Length 127;  
 Best Local Similarity 89.8%; Pred. No. 2.65e-53;  
 Matches 114; Conservative 9; Mismatches 4; Indels 0; Gaps 0;  
 Db 1 mvstpqflglvllcfcgtrcdiqtqtsslaslsgdrvtiscasqgsniynwyqkqp 60  
 Qy 1 MVSSAQFLGLLLCFCGTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKQP 60  
 Db 61 dgtvkllydtrihsgvprsfsgsgtdyaltisnleqediasyfcqggytpptfgg 120  
 Qy 61 DGTIKLLIYTRSLHSGVPSRFSGSGTDYSLTINNLEQEDATYFCQGNTLPYTFGG 120  
 Db 121 gtkleik 127  
 Qy 121 GTKLEIN 127

RESULT 7  
 ID R12359 standard; Protein; 127 AA.  
 AC R12359;  
 DT 15-AUG-1991 (first entry)  
 DE Light (kappa) chain variable region of murine 1C11 immunoglobulin.  
 KW Chimeric antibodies; Immunoconjugates; HIV; AIDS.  
 OS Mus musculus.  
 PN W09107493-A.  
 PD 13-NOV-1990; U06615.  
 PF 13-NOV-1989; US-433730.  
 PR (XOMA-) XOMA CORP.  
 PA (GREC) GREEN CROSS CORP.  
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;  
 DR WPI; 91-178044/24.  
 DR N-PSDB; Q12061.  
 PT New chimeric mouse-human antibodies - used to detect, kill and  
 PT remove HIV-1 antigen from sample  
 PS Disclosure; fig 13; 107pp; English.

CC This is the light (kappa)- chain variable (V) region of a mouse  
 CC monoclonal antibody (MAb), 1C11, and is specific for an HIV-1  
 CC viral antigen. It is used in the construction of a chimeric  
 CC MAb comprising heavy and light chains having murine V regions  
 CC and human C regions. The chimeric MABs are more effective than  
 CC murine MAB 1C11 since they have an increased compatibility in  
 CC humans. The heavy and light chain V-regions are joined by  
 CC manipulating their respective joining (J) regions, to generate  
 CC restriction enzyme recognition sites. The chimeric MABs can be  
 CC used as immunoconjugates, in association with e.g. toxins for HIV  
 CC treatment. They can also be used in diagnosis of HIV.  
 CC See also Q12056-60 and Q12062-63.  
 SQ Sequence 127 AA;

Query Match 90.0%; Score 818; DB 2; Length 127;  
 Best Local Similarity 89.0%; Pred. No. 1.09e-52;  
 Matches 113; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
 Db 1 mmsaqlglvllcfcgtrcdiqtqtsslaslsgdrvtiscasqgsniynwyqkqp 60  
 Qy 1 MVSSAQFLGLLLCFCGTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKQP 60  
 Db 61 dgtvkllydtrihsgvprsfsgsgtdyaltisnleqediasyfcqggytpptfgg 120  
 Qy 61 DGTIKLLIYTRSLHSGVPSRFSGSGTDYSLTINNLEQEDATYFCQGNTLPYTFGG 120  
 Db 121 gtkleik 127  
 Qy 121 GTKLEIN 127

RESULT 8  
 ID R12237 standard; Protein; 126 AA.  
 AC R12237;  
 DT 19-AUG-1991 (first entry)  
 DE Mouse MAB 1C11 L chain V region.  
 KW HIV-1; chimera.  
 OS Mus sp.  
 PN W09107494-A.  
 PD 30-MAY-1991.  
 PF 13-NOV-1990; U06627.  
 PR 13-NOV-1989; US-433703.  
 PA (XOMA-) Xoma Corp.  
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;  
 DR WPI; 91-178106/24.  
 DR N-PSDB; Q12017.  
 PT New chimeric mouse human antibodies - used in treatment, diagnosis  
 PT and prophylaxis of HIV infections.  
 PS Disclosure; Fig 13; 108pp; English.  
 CC The mouse VL gene product may be used to produce chimeric mouse-  
 CC human Abs against HIV-1 comprising human Ig constant regions and  
 CC murine variable regions. These novel sequence are useful in  
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be  
 CC produced by a bacterial, yeast or mammalian expression system.  
 SQ Sequence 126 AA;

Query Match 89.9%; Score 817; DB 2; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 1.30e-52;  
 Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 Db 1 mmsaqlglvllcfcgtrcdiqtqtsslaslsgdrvtiscasqgsniynwyqkqp 60  
 Qy 1 MVSSAQFLGLLLCFCGTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKQP 60

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KW Ig; immunoglobulin; promoter; enhancer.

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KW Ig; immunoglobulin; promoter; enhancer.

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OS Mus musculus.  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= eig\_peptide  
PW AU9346181-A.  
PD 17-MAR-1994.  
PR 07-SEP-1992; JP-238452.  
PA (KYOM ) KYOMA HAKKO KOGYO KK.  
PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;  
PI Shitara K;  
DR WPI; 94-126857/16.  
DR N-PSDB; Q45438.  
PT Humanised antibody specific for ganglioside GM2 - used for  
PT producing a cytotoxic effect on cancers such as melanoma,  
PT neuroblastoma and glioma.  
PS Reference example 2; Page 115-116; 191pp; English.  
CC Example 2 describes the construction of the vector pChi641HA1  
CC for chimeric human antibody H chain expression.  
CC mRNA from mouse anti-GD3 monoclonal Ab KM641-producing cells  
CC was isolated and KM641 H and L chain cDNAs isolated.  
CC The base sequences of the Ig variable regions in KM641  
CC H chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2)  
CC are given in Q45438-39. A KM641-derived chimeric human  
CC Ab H chain expression vector was constructed by joining  
CC the H chain variable region gene from pKM641HA3 to a  
CC vector for chimeric human Ab H chain expression using  
CC the synthetic DNAs given in Q63439 and Q63440.  
SQ Sequence 128 AA;

Query Match 86.5%; Score 786; DB 10; Length 128;  
Best Local Similarity 84.3%; Pred. No. 3.16e-50;  
Matches 107; Conservative 12; Mismatches 8; Indels 0; Gaps 0;  
  
Db 1 mmsaaqflgllllcfqtrcdiqtatasepalslgdrvtiscsasqdiynylnwyqkq 60  
Qy 1 MYSSAQFLGILLCLLCFQGTGTRCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKQP 60  
  
Db 61 dgtvkllyfsenlhsgvparfsagsgtgytltisnleqdiatyfchqysklptegg 120  
Qy 61 DGTIKLIIYTSRLHSGVPSRFSGSGCTDYSLTINWLEQDIATYFCQGGNTLPYFEGG 120  
  
Db 121 gtleik 127  
Qy 121 GTRLEIN 127

RESULT 12  
ID R30768 standard; protein; 107 AA.  
AC R30768;  
DT 12-MAY-1993 (first entry)  
DE Murine anti-CD3 Mab UCHT1 light chain variable domain.  
KW Humanisation; rapid; monoclonal antibody; muxCD3.  
OS Mus musculus.  
PN W09222653-A.  
PD 23-DEC-1992.  
PF 15-JUN-1992; U05126.  
PR 14-JUN-1991; US-715272.  
PA (GETH ) GENENTECH INC.  
PI Carter PJ, Presta IG.  
DR WPI; 93-018139/02.  
PT Humanisation of antibodies - by molecular modelling of the variable  
PT domains and alteration by gene conversion mutagenesis  
PS Disclosure; Fig 5; 126pp; English.

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CC The sequence is that of the light chain variable domain of murine  
CC anti-CD3 monoclonal antibody UCHT1 (muxCD3, Shalaby 1992).  
SQ Sequence 107 AA;  
  
Query Match 77.9%; Score 708; DB 6; Length 107;  
Best Local Similarity 92.5%; Pred. No. 3.06e-44;  
Matches 99; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
  
Db 1 digmtqtteslaelgdrvtiscraeqdiynylnwyqkpdqgtvkllytserlhsgvps 60  
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKPDGTIKLIIYTSRLHSGVPS 80  
  
Db 61 kfsgsgtdysltisnleqdiatyfchqysklptfaggtkklk 107  
Qy 81 RFGSGSGTDYSLTINWLEQDIATYFCQGGNTLPYFEGGKLEIN 127

RESULT 13  
ID R60206 standard; Protein; 302 AA.  
AC R60206;  
DT 14-MAR-1995 (first entry)  
DE Bispecific CD3-L6Fvlg antibody derivative.  
KW fusion protein; recombinant bispecific single chain antibody;  
KW helical peptide linker; anti-L6 antibody; tumour cell antigen;  
KW anti-CD3 antibody; variable region.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= L6\_VL leader  
FT Region 24..271  
FT /label= CD3\_VL-VH fusion  
FT Region 134..148  
FT /label= (Gly4Ser)3 linker  
FT Region 272..274  
FT /label= hinge 275..302  
FT Region  
FT /label= Fv helical linker  
PW EP-610046-A.  
PD 10-AUG-1994.  
PF 31-JAN-1994; 300692.  
PR 01-FEB-1993; US-013420.  
PR 13-SEP-1993; US-121054.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PI Bajorath J, Fell PH, Gilliland LK, Hayden MS, Ledbetter JA;  
PI Linsley PS;  
DR WPI; 94-250885/31.  
DR N-PSDB; Q81076.  
PT Expression vector encoding bispecific fusion protein - having  
PT binding domains for separate targets joined by helical peptide,  
PT useful e.g. for diagnosis and treatment  
PS Example 1; Fig 11 and Page 29-31; 50pp; English.  
CC The VL and VH sequences of the anti-CD3 hybridoma G19-4 were  
CC amplified by PCR methods. A gene fusion was constructed from the  
CC two amplified domains and a (Gly4Ser)3 linker. The amino  
CC terminus of the VL-VH fusion cassette was fused at the SalI site to  
CC the L6 light chain variable region leader peptide and the  
CC carboxy-terminus was fused directly to the hinge region of the Fc  
CC domain at the BclI site and/or to a short "helical" peptide linker  
CC to construct the bispecific CD3-L6Fvlg antibody derivative. The  
CC variable regions for L6 were fused in frame to the opposite end of  
CC the helical linker (not included in R60206).  
SQ Sequence 302 AA;

Query Match 76.3%; Score 694; DB 11; Length 302;

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13

Best Local Similarity 93.3%; Pred. No. 3.61e-43;  
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Db 24 diqmqttslasaslgdrvtisrcasqdirnylnwyqkqkdgvtklllytstlhagvps 83  
Qy 21 DIQMTQTTSLSASLGDRVTISCRASQDISSYLNWYQKQKPDGTIKLLIYTSRLHSGVPS 80  
Db 84 rfsgegsqtdysltianlqpediatyfcqggntlpwtfgggtkl 127  
Qy 81 RFSGSGSTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGTKL 124

RESULT 14

ID R30776 standard; protein; 214 AA.  
AC R30776;  
DT 12-MAY-1993 (first entry)  
DE H52L6-158 murine anti-CD18 antibody light chain.  
KW Humanisation; rapid; monoclonal antibody.  
OS Mus musculus.  
PN W09222653-A.  
PD 23-DEC-1992.  
PF 15-JUN-1992; U05126.  
PR 14-JUN-1991; US-715272.  
PA (GETH ) GENENTECH INC.  
PI Carter PJ, Presta LG.  
DR WPI; 93-018139/02.  
PT Humanisation of antibodies - by molecular modelling of the variable  
PT domains and alteration by gene conversion mutagenesis  
PS Disclosure; Fig 68; 126pp; English.  
CC The sequence is that of the light chain of murine anti-CD18  
CC antibody H52L6-158.  
SQ Sequence 214 AA;

Query Match 75.5%; Score 686; DB 6; Length 214;  
Best Local Similarity 88.8%; Pred. No. 1.48e-42;  
Matches 95; Conservative 10; Mismatches 2; Indels 0; Gaps 0;  
Db 1 dvqmqttslasaslgdrvtincrasqdirnylnwyqkqkngvtklllytstlhagvps 60  
Qy 21 DIQMTQTTSLSASLGDRVTISCRASQDISSYLNWYQKQKPDGTIKLLIYTSRLHSGVPS 80  
Db 61 rfsgegsqtdysltianlqpediatyfcqggntlpwtfgggtkveik 107  
Qy 81 RFSGSGSTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGTKLEIN 127

RESULT 15

ID R47207 standard; Protein; 129 AA.  
AC R47207;  
DT 09-AUG-1994 (first entry)  
DE Human/murine IL-1 chimeric antibody VL.  
KW Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;  
KW light; L; chain; constant; region; variable; mouse; anti-human;  
KW graft; CDR; complementarity determining region; heavy; H;  
KW inflammatory disease; arteriosclerosis; detection;  
KW diffused intravascular coagulation; leukemia.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /note= "Signal peptide"  
FT Protein 21..129  
FT /note= "Mature protein"  
PN W09402627-A.  
PD 03-FEB-1994.

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PF 08-JUL-1993; J00941.  
PR 16-JUL-1992; JP-189248.  
PA (SAKA ) OTSUKA PHARM CO LTD.  
PI Hirai Y, Nishida T, Onoto Y, Owens RJ;  
DR WPI; 94-048885/06.  
DR N-PSDB; 056068.  
PT Mouse/human chimeric antibody against human interleukin-1 - for  
PT treatment of diseases in which production of interleukin-1 is  
PT abnormal, and for diagnostic imaging of interleukin-1 production  
PT sites in vivo  
PS Claim 2; Fig 10; 58pp; Japanese.  
CC The sequences given in R47205-08 represent the light and heavy chain,  
CC variable and constant regions of a chimeric recombinant antibody  
CC against human interleukin-1 (IL-1). The antibody has a light (L)  
CC chain in which the constant region is that of a human antibody and  
CC the variable region is from a mouse anti-human IL-1 antibody or is a  
CC mouse-human graft containing the CDR regions of mouse anti-human IL-1  
CC antibody, and a heavy (H) chain in which the constant region is that  
CC of a human antibody and the variable region is from a mouse anti-human  
CC IL-1 antibody or is a mouse-human graft containing the CDR regions of  
CC mouse anti-human IL-1 antibody,. The chimeric antibody is used to  
CC treat diseases in which abnormal amounts of IL-1 are produced, eg.  
CC inflammatory disease, arteriosclerosis, diffused intravascular  
CC coagulation or leukemia. It can also be labelled and used for  
CC diagnostic imaging of IL-1 producing sites in vivo.  
SQ Sequence 129 AA;

Query Match 74.9%; Score 681; DB 9; Length 129;  
Best Local Similarity 73.0%; Pred. No. 3.56e-42;  
Matches 92; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

Db 1 msvptqvlglillwltardcdiqmtqpslsasvgrvtitcrtsqdimnlwnyqqtq 60  
Qy 1 WYSSAQFLGILLLLCFQCTRCDIQMTQTTSLSASLGDRVTISCRASQDISSYLNWYQKQP 60  
Db 61 gkapklllytserlhsgvpsrfsgegsqtdyftisslqpediatyvcqgktpwtfgq 120  
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGSTDYSLTINNLEQEDIATYFCQGGNTLPYTFGG 120  
Db 121 gtlqi 126  
Qy 121 GTKLEI 126

Search completed: Mon Jul 8 08:33:13 1996  
Job time : 17 secs.



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W P E R E A (TM)

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MPorch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:34:20 1996; MasPar time 8.84 Seconds  
Tabular output not generated. 391.433 Million cell updates/sec

Title: >US-08-137-117B-31  
Description: (1-137) from US08137117B.pep  
Perfect Score: 1002  
Sequence: 1 MRVLILWLWLTAFPCILSDV.....LARTTMDYWGQTSVTWSS 137

Scoring table: PAM 150  
Gap 11

Searched: 82306 seqs, 25270970 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir46

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1  
13:unrev2

Statistics: Mean 42.150; Variance 133.880; scale 0.315

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	835	83.3	149	5	S30752	Ig heavy chain precu	3.01e-89
2	828	82.6	135	5	P10100	Ig heavy chain precu	2.46e-88
3	774	77.2	134	5	B24672	Ig heavy chain precu	2.61e-81
4	768	76.6	116	2	HVMS1B	Ig heavy chain precu	1.57e-80
5	745	74.4	137	2	AVMS35	Ig heavy chain precu	1.51e-77
6	744	74.3	136	5	S07637	Ig heavy chain V reg	2.04e-77
7	736	73.5	119	11	C53285	monoclonal antibody	2.22e-76
8	729	72.8	117	11	I28195	Ig heavy chain V reg	1.79e-75
9	722	72.1	116	2	HVMS31	Ig heavy chain precu	1.44e-74
10	707	70.6	116	5	S38718	Ig heavy chain V reg	1.25e-72
11	673	67.2	115	11	D33932	Ig mu chain precursu	3.06e-68
12	672	67.1	106	5	S26464	Ig heavy chain V reg	4.11e-68

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13	661	66.0	121	13	S37200	Ig heavy chain V reg	1.07e-66
14	653	65.2	117	13	S23599	Ig alpha chain (MOPC)	1.15e-65
15	650	64.9	119	2	HVMS73	Ig heavy chain precu	2.79e-65
16	645	64.4	115	11	F25114	Ig heavy chain V reg	1.23e-64
17	639	63.8	119	5	E25114	Ig heavy chain V reg	7.23e-64
18	630	62.9	119	11	C25114	Ig heavy chain V reg	1.03e-62
19	623	62.2	123	11	S24771	Ig heavy chain - mou	8.17e-62
20	613	61.2	104	5	S26467	Ig heavy chain V reg	1.56e-60
21	609	60.8	113	2	G2MS60	Ig heavy chain V reg	5.08e-60
22	609	60.8	119	11	D25114	Ig heavy chain V reg	5.08e-60
23	608	60.7	120	11	A25114	Ig heavy chain V reg	6.83e-60
24	582	58.1	100	5	S14485	Ig heavy chain V reg	1.44e-56
25	575	57.4	147	13	S13519	Ig heavy chain V reg	1.12e-55
26	574	57.3	102	11	S14488	Ig heavy chain V reg	1.51e-55
27	572	57.1	101	5	S14484	Ig heavy chain V reg	2.71e-55
28	570	56.9	152	13	S25476	Ig heavy chain V reg	4.88e-55
29	565	56.4	102	11	S14486	Ig heavy chain V reg	2.11e-54
30	553	55.2	137	13	S31676	Ig heavy chain V reg	7.11e-53
31	553	55.2	139	5	A32456	Ig heavy chain precu	7.11e-53
32	552	55.1	102	11	S14487	Ig heavy chain V reg	9.53e-53
33	549	54.8	155	5	S31511	Ig heavy chain - hum	2.29e-52
34	546	54.5	138	11	S54225	Ig mu heavy chain V	5.52e-52
35	546	54.5	139	13	S31586	Ig heavy chain V reg	5.52e-52
36	544	54.3	155	5	S31512	Ig heavy chain - hum	9.90e-52
37	537	53.6	118	5	S24443	Ig heavy chain V reg	7.66e-51
38	533	53.2	118	5	S20780	Ig heavy chain V reg	2.46e-50
39	529	52.8	141	11	S54236	Ig mu heavy chain V	7.92e-50
40	528	52.7	135	13	S21681	Ig heavy chain precu	1.06e-49
41	528	52.7	141	11	S54226	Ig mu heavy chain V	1.06e-49
42	526	52.5	117	5	E34964	Ig heavy chain precu	1.90e-49
43	526	52.5	140	11	S54239	Ig mu heavy chain V	1.90e-49
44	525	52.4	112	13	S13685	Ig heavy chain V reg	2.54e-49
45	524	52.3	140	5	A24770	hypothetical hybrid	3.40e-49

ALIGNMENTS

RESULT 1  
ENTRY S30752 #type complete  
TITLE Ig heavy chain precursor V region - mouse  
ORGANISM #formal\_name Mus musculus #common name house mouse  
DATE 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Sep-1995  
ACCESSIONS S30752  
REFERENCE S30751  
#authors Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.  
#journal Nucleic Acids Res. (1987) 15:5496  
#title Improved RNA sequencing method to determine immunoglobulin mRNA sequence.  
#accession S30752  
#molecule\_type mRNA  
#residues 1-149 #label GRA  
#crosses-references EMBL:X05878  
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS immunoglobulin  
FEATURE  
138-149 #domain C region (C-gamma 2b) (fragment) #status predicted #label CRE  
SUMMARY  
#length 149 #molecular-weight 16635 #checksum 9814  
Query Match 83.3%; Score 835; DB 5; Length 149;  
Best Local Similarity 84.7%; Pred. No. 3.01e-89;  
Matches 116; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Db	1	mrvliliclvta	fgilsdvql	gesgpdil	vkpsgsia	lctctv	gysitsy	tw	hwi	rffp	60
Qy	1	MRVLILICLVTA	FGILSDVQL	GESGPDIL	VKPSGSIA	LCTCTV	GYSITSY	TW	HWI	RFFP	60
Db	61	gnkiewmay	ihyegntd	fnfpel	karisitr	dknqff	liqlnsvt	aed	taty	cary	120
Qy	61	GNKIEWMAY	IHYEGNTD	FNFPEL	KARISITR	DKNQFF	LIQLNSVT	AED	TATY	CARY	120
Db	121	yyamdy	wqgqts	vtvs	137						
Qy	121	YYAMDY	WQGQTS	VTVS	137						

```

ENTRY 2
TITLE Ig heavy chain precursor V region (40-140) - mouse
FORMAL_NAME Mus musculus #common_name house mouse
DATE 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
12-Apr-1995
ACCESSIONS PL0100 #type complete
REFERENCE PL0100
AUTHORS Near, R.I.; Haber, E.
JOURNAL Mol. Immunol. (1989) 26:371-382
TITLE Characterization of the heavy and light chain immunoglobulin
variable region genes used in a set of anti-digoxin
antibodies.
CROSS-REFERENCES MUID:89238344
ACCESSION PL0100
MOLECULE_TYPE DNA
RESIDUES 1-135 #label NEA
EXPERIMENTAL_SOURCE strain A/J
NOTE the VH40-140 gene segment is classified as a member of
the 36-60 VH gene family

```

```

GENETICS
#introns
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
1-18
19-115
117-118
119-135
SUMMARY
#domain signal sequence #status predicted #label SIG\
#domain V segment #status predicted #label VRE\
#domain D segment #status predicted #label DRE\
#domain J segment #status predicted #label JRE
#length 135 #molecular-weight 15303 #checksum 9859
Query Match 82.6%; Score 828; DB 5; Length 135;
Best Local Similarity 84.7%; Pred. No. 2,46e-88;
Matches 116; Conservative 9; Mismatches 9; Indels 3; Gaps 2;

```

Db	1	mrvllllwlfafpgglsdqlqespglvpkpsqslctctwtgysitsdyawsirfqp	60
		:     :     :     :     :     :     :     :	
Qy	1	MRVLLILLWLFAPGGLSDQLQESGPLVKPSQSLSLCTVTGYITSDHAMSWIRQFP	60
Db	61	gnrlewmgyityngytynpnlkerfafrtdeksnqlflqlsvttedatyyvcaryd-	119
		:     :     :     :     :     :     :     :     :	
Qy	61	GKLEWMGYISYSGITTYNPSLKSRTSITRDTSKNQFFLQLNSVTGTSTYYCARSLAR	120
Db	120	-y-fdwaggtltlvaa	134
		:	
Qy	121	TTAMDYWGQGSTSVTVSS	137

RESULT	ENTRY	3
TITLE	B24672	#type complete
ORGANISM	Ig heavy chain precursor V region (VGM3-2)	- mouse
	#formal name Mus musculus	#common name house mouse

```

DATE      19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change
          31-Dec-1993
ACCESSION B24672
REFERENCE  A91022
#authors  Winter, E.; Radbruch, A.; Krawinkel, U.
#journal  EMBO J. (1985) 4:2861-2867
#cross-references MUID:86055722
#accession B24672
#molecule_type DNA
#residues  1-134 #label WIN
#note      this sequence was determined from the differentiated
           gene

```

```

GENETICS
  #introns 15/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
  19-134 #product Ig heavy chain V region VGM3-2 #label VAT
SUMMARY #length 134 #molecular-weight 15254 #checksum 6268

Query Match 77.2%; Score 774; DB 5; Length 134;
Best Local Similarity 82.5%; Pred. No. 2.61e-81;
Matches 113; Conservative 3; Mismatches 18; Indels 3; Gaps 2;

Db 1 mrvlllclftaagildcvlcesgpdvlkpsqslstctvtgfitgysvhwirgfp 60
Qy 1 MRVLLLMFTAFPGILSDVQLQESGPGVLKPSQSLSCTCTVTGYSITDSHWIRQFP 60

Db 61 gnklemwyihyagstynpnlksrisitrdtsknfflqlnsvttedatycaryvd- 119
Qy 61 GNKLEMWGYSYSGITTYNPSLKSRSITRDTSKNFFLQNSVTTGDTSTYYCARSLAR 120

Db 120 -y-faywagggtlvtsea 134
Qy 121 TTAMDYWGQGTSTVTVSS 137

```

RESULT	4
ENTRY	
TITLE	HVMS1B #type complete
ORGANISM	Ig heavy chain precursor V region (I43) - mouse
DATE	#formal_name Mus musculus #common name house mouse 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Feb-1995
ACCESSIONS	JT0508
REFERENCE	JT0501
#authors	Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
#journal	J. Exp. Med. (1989) 169:2007-2019
#title	Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.

```

#cross-references MUID:89279149
#accession JT0508
#molecule_type mRNA
#residues 1-116 #label LEV
#experimental_source strain BAIB/cJ
#note amino acid sequence is not given
#note this sequence belongs to the VH3660 subfamily
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
1-18 #domain signal sequence #status predicted #label SIG
19-116 #product Ig heavy chain V region (IB43) #status
      predicted #label MATV
33-116 #domain immunoglobulin homology #label IMM
#length 116 #molecular-weight 13158 #checksum 1197
SUMMARY

```

```

#cross-references MUID:7410779
#accession A93787
#molecule_type protein
#residues 19-52,'K','53-75','BYGB','80-101','D','103-106','ZB','109-122,
124-137 ##label FRA

REFERENCE      A94684
#authors      Hood, L.; Margolies, M.; Givol, D.; Zakut, R.
#citation     unpublished results, cited by Padlan, E.A., Davies, D.R.,
              Pecht, I., Givol, D., and Wright, C., Cold Spring Harbor
              Symp. Quant. Biol. 41, 627-637, 1977
#contents    annotation; revision to residue 53
COMMENT      This alpha chain was isolated from a myeloma protein that has
              anti-dinitrophenyl activity.

GENETICS
#introns     15/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
1-18          #domain signal sequence #status experimental #label SIG
19-136       #product Ig heavy chain V region (MOPC 315) #label MATV
33-116       #domain immunoglobulin homology #label IMM
SUMMARY      #length 137 #molecular-weight 15399 #checksum 2186

Query Match           74.4%; Score 745; DB 2; Length 137;
Best Local Similarity 73.7%; Pred.No. 1.5le-77;
Matches 101; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Db 1 mkvlslllyltaipgimdvqlgespglivkpsqslscvtsgysitegyfwnwirqfp 60
   |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Qy 1 MRVILLMLTFAPGILSDVLQESGPVLVKPSQSLSLCVTVCYSTTSDHMSWIRQFP 60

Db 61 qnklewlfkgfydsgnypsknrsvitrdtsengfflklnsvttedatycagdnhd 120
   |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| :
Qy 61 GNKLEHWGVYSIGITTPNSLKSRIISITRDSKNQFFQLNLSVTGGDTSTTYCARSLAR 120

Db 121 Lyfydywgqgttlvs 137
   |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| :
Qy 121 TTANDYWGQGTSVTVSS 137

RESULT 6
ENTRY S07637 #type complete
TITLE Ig heavy chain V region (PTE.02) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
        28-Oct-1994
ACCESSIONS S07637
REFERENCE S07637
#authors Urakov, D.N.; Deev, S.M.; Polyakovskiy, O.L.
#journal Nucleic Acids Res. (1989) 17:9491
#title The structure of the expressible VH gene from a hybridoma
        producing monoclonal antibodies against porcine
        transferrin.
#cross-references MUID:90067954
#accession S07637
#molecule_type DNA
#residues 1-136 ##label URA
#cross-references EMBL:X16740
##note the authors translated the codon TAT for residue 112 as
        Ile, TAC for residue 113 as Ile, and TAC for residue
        120 as Thr

GENETICS
#introns     15/3
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY      #length 136 #molecular-weight 15307 #checksum 182

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\*\*\*\*\*  
MParch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Mon Jul 8 08:33:31 1996; MasPar time 4.97 Seconds  
Tabular output not generated.  
Title: >US-08-137-117B-31  
Description: (1-137) from US08137117B.pep  
Perfect Score: 1002  
Sequence: 1 MRVLILWLFTAFGILSDV.....LARTTAMDYWGQGTSTVTVSS 137  
Scoring table: PAM 150  
Gap 11  
Searched: 43470 seqs, 15335248 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Database: swiss-prot31  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8  
Statistics: Mean 42.978; Variance 84.975; scale 0.506  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.  
SUMMARIES  
Result Query  
No. Score Match Length DB ID Description Pred. No.  
1 768 76.6 116 4 HV61\_MOUSE IG HEAVY CHAIN PRECUR 2.01e-130  
2 745 74.4 137 4 HV46\_MOUSE IG HEAVY CHAIN PRECUR 1.21e-125  
3 722 72.1 116 4 HV60\_MOUSE IG HEAVY CHAIN PRECUR 7.13e-121  
4 650 64.9 117 4 HV62\_MOUSE IG HEAVY CHAIN PRECUR 5.31e-106  
5 609 60.8 113 4 HV47\_MOUSE IG HEAVY CHAIN V REGI 1.40e-97  
6 499 49.8 144 4 HV43\_MOUSE IG HEAVY CHAIN PRECUR 3.37e-75  
7 481 48.0 117 4 HV26\_HUMAN IG HEAVY CHAIN V-II R 1.40e-71  
8 481 48.0 135 4 HV02\_XENLA IG HEAVY CHAIN PRECUR 1.40e-71  
9 469 46.8 146 4 HV21\_HUMAN IG HEAVY CHAIN PRECUR 3.59e-69  
10 455 45.4 115 4 HV44\_MOUSE IG HEAVY CHAIN PRECUR 2.28e-66  
11 442 44.1 116 4 HV45\_MOUSE IG HEAVY CHAIN PRECUR 8.99e-64  
12 442 44.1 136 4 HV01\_XENLA IG HEAVY CHAIN PRECUR 8.99e-64  
13 438 43.7 121 4 HV2E\_HUMAN IG HEAVY CHAIN V-II R 5.64e-63

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14 429 42.8 136 4 HV16\_MOUSE IG HEAVY CHAIN PRECUR 3.48e-61  
15 425 42.4 129 4 HV2F\_HUMAN IG HEAVY CHAIN V-II R 2.17e-60  
16 423 42.2 119 4 HV2C\_HUMAN IG HEAVY CHAIN V-II R 5.41e-60  
17 420 41.9 119 4 HV3L\_HUMAN IG HEAVY CHAIN V-II R 2.13e-59  
18 414 41.3 139 4 HV07\_MOUSE IG HEAVY CHAIN PRECUR 3.29e-58  
19 412 41.1 122 4 HV3H\_HUMAN IG HEAVY CHAIN V-II R 8.20e-58  
20 409 40.8 122 4 HV3C\_HUMAN IG HEAVY CHAIN V-II R 3.21e-57  
21 408 40.7 117 4 HV42\_MOUSE IG HEAVY CHAIN V REGI 5.07e-57  
22 407 40.6 117 4 HV54\_MOUSE IG HEAVY CHAIN PRECUR 7.99e-57  
23 407 40.6 140 4 HV02\_MOUSE IG HEAVY CHAIN PRECUR 7.99e-57  
24 406 40.5 115 4 HV3F\_HUMAN IG HEAVY CHAIN V-II R 1.26e-56  
25 404 40.3 117 4 HV55\_MOUSE IG HEAVY CHAIN PRECUR 3.13e-56  
26 403 40.2 122 4 HV3A\_HUMAN IG HEAVY CHAIN V-II R 4.93e-56  
27 402 40.1 137 4 HV11\_MOUSE IG HEAVY CHAIN PRECUR 7.76e-56  
28 398 39.7 119 4 HV40\_MOUSE IG HEAVY CHAIN V REGI 4.78e-55  
29 396 39.5 115 4 HV3S\_HUMAN IG HEAVY CHAIN V-II R 1.18e-54  
30 392 39.1 116 4 HV05\_CARAU IG HEAVY CHAIN PRECUR 7.26e-54  
31 392 39.1 117 4 HV14\_MOUSE IG HEAVY CHAIN PRECUR 7.26e-54  
32 391 39.0 119 4 HV37\_MOUSE IG HEAVY CHAIN V REGI 1.14e-53  
33 390 38.9 121 4 HV3J\_HUMAN IG HEAVY CHAIN V-II R 1.80e-53  
34 389 38.8 117 4 HV41\_MOUSE IG HEAVY CHAIN V REGI 2.83e-53  
35 387 38.6 119 4 HV38\_MOUSE IG HEAVY CHAIN V REGI 6.99e-53  
36 386 38.5 125 4 HV2D\_HUMAN IG HEAVY CHAIN V-II R 1.10e-52  
37 384 38.3 116 4 HV3T\_HUMAN IG HEAVY CHAIN V-II R 2.71e-52  
38 384 38.3 120 4 HV2B\_HUMAN IG HEAVY CHAIN V-II R 2.71e-52  
39 383 38.2 117 4 HV3C\_HUMAN IG HEAVY CHAIN PRECUR 4.26e-52  
40 382 38.1 117 4 HV58\_MOUSE IG HEAVY CHAIN PRECUR 6.70e-52  
41 382 38.1 147 4 HV2H\_HUMAN IG HEAVY CHAIN PRECUR 6.70e-52  
42 380 37.9 142 4 HV01\_RAT IG HEAVY CHAIN PRECUR 1.65e-51  
43 376 37.5 114 4 HV3B\_HUMAN IG HEAVY CHAIN V-II R 1.01e-50  
44 376 37.5 117 4 HV17\_MOUSE IG HEAVY CHAIN V REGI 1.01e-50  
45 376 37.5 118 4 HV39\_MOUSE IG HEAVY CHAIN V REGI 1.01e-50

ALIGNMENTS

RESULT 1  
ID HV61\_MOUSE STANDARD; PRT; 116 AA.  
AC P18532;  
DT 01-NOV-1990 (REL. 16, CREATED)  
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
DE IG HEAVY CHAIN PRECURSOR V REGION (1B43).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/CJ;  
RM 89279149  
RA LEVY N.S., WALPIERO U.V., LEBEQUE S.G., GEARHART P.J.;  
RL J. EXP. MED. 169:2007-2019(1989).  
CC -!- THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.  
DR PIR; J0508; HVMSIB.  
DR HSP; P01825; IBAF.  
KW IMMUNOGLOBULIN V REGION; SIGNAL.  
FT SIGNAL 1 18  
FT CHAIN 19 116 IG HEAVY CHAIN V REGION (1B43).  
FT DOMAIN 19 48 FRAMEWORK 1.  
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 54 67 FRAMEWORK 2.  
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 85 116 FRAMEWORK 3.  
FT DISULFID 40 114 BY SIMILARITY.





QY	1	MRLVLLWLTAFPPGILLSDVQLQESGVLVLPKPSOSLSLTCTVTGYTSIDHAWSNIQFP	60
Db	61	gnkIEWgYISydgngnynpSLkriEtrtdsknqffklnsvrtedatyyear	116
QY	61	gnkLEWngYISyGITTTPNPslkRSIGITRDTsknqffQLINSVTTGDTSTYYCAR	116

	RESULT	4						PRT;	117 AA.	
ID	HV62 MOUSE STANDARD;									
AC	P18533;									
DT	01-NOV-1990 (REL. 16, CREATED)									
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)									
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)									
DE	IG HEAVY CHAIN PRECURSOR V REGION ('733).									
OS	MUS MUSCULUS (MOUSE) .									
OC	EUKARYOTA; METAZOA;									
CC	EUTHERIA; RODENTIA.									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN=BALB/CJ;									

RA	LEVY N.S., MALIPIERO U.V., LEBECQUE S.G., GEARHART P.J.;
RL	J. EXP. MED. 169:2007-2019(1989).
DR	PIR; JT0510; HVM573.
DR	HSP; P01825; IBAF.
KW	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL 1 18
FT	CHAIN 19 117 IG HEAVY CHAIN V REGION (733).
FT	DISULFID 40 115 BY SIMILARITY.
FT	NON TER 117 117
SO	SEQUENCE 117 AA: 13223 MW: 77503 CN:

Query Match 64.9%; Score 650; DB 4; Length 117;  
Best Local Similarity 74.4%; Pred. No. 5.31e-106;  
Matches 87; Conservative 17; Mismatches 12; Indels 1; Gaps 1;

```
Db      1 mkmftlllyltvvpqilsvqlgespglvkpsqsalctvtgisittgnyrwswirgf 60
        ::: || |: | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      1 MRVLLILWFATPPGILLSDVQLQESGPVLKPSQSLSLTCTVTGYSTLSDIAWSIIRGF 59
```

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61 Db pgnklewigyysaitysnpskrtitrdtsknqflemnsltaedtatyyca 117
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
60 Qv PGKLEWGMGYISYSGITTYNPSLKSRIISITRTSKNOFFLOINSVTGDTSTYYCAR 116

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RESULT	5	STANDARD;	PRT;	113 AA.
ID	HV47 MOUSE			
AC	p01823;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN V REGION (36-60).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			

CC CC -1- THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE MONOCLONAL ANTIBODY OF THE IGGA SUBCLASS. IT REPRESENTS A SECOND IDIOTYPE FAMILY

CC	CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF STRAIN A/J MICE.
PIR; A02098; C2M560.	
DR	
DR	
DR	
HSP; P01875; 1HEM.	
KW	
IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.	
NON TER	113 113
113	113
SQ	
SEQUENCE	113 AA: 12734 MW: 78306 CN:

Query Match	60.8%;	Score 609;	DB 4;	Length 113;
Best Local Similarity	78.2%;	Pred. No. 1.40e-97;		
Matches	93;	Conservative 10;	Mismatches 10;	Indels 6; Gaps 5;
Db	1	evlqsgslvlpkstlscvtgdsitcdy-wwirfkpgnklehmcylsygstyv 59		
	:			
	:			
QY	19	DVQLQSGPVLVLPQSGLSLCTVTGYSTSDHAWSIHQFFGNKLEWMCYISYGITY 78		
	:			
	:			
Db	60	npalkeisrtdrshngyqlnsvtsedatyyct-sl--f--ywgqgtltvtva 113		
	:			
	:			
QV	79	NPISAKRSISITROTSGNOFFIQLNLSVTGDSITTYCARSILATTDAMDVGQGSYTVSS 137		
	:			
	:			

RESULT	6	
ID	HVA3 MOUSE	STANDARD; PRT; 144 AA.
AC	P01819;	
DT	21-JUL-1986 (REL. 01, CREATED)	
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)	
DE	IG HEAVY CHAIN PRECURSOR V REGION (MOPC 141).	
OS	MUS MUSCULUS (MOUSE).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	
RN	{1}	
RP	SEQUENCE FROM N. A.	
RM	81012133	
RL	SAKANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.;	
RA	NATURE 286:676-683(1980).	
CC	-!- THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE	
CC	ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.	
CC	PIR; A02094; GZMS14.	
DR	HSSP; P011772; 1FDL.	
KW	IMMUNOGLOBULIN V REGION; SIGNAL.	
FT	FT SIGNAL 1 19	
FT	CHAIN 20 144	IG HEAVY CHAIN V REGION (MOPC 141)
FT	NON TER 144 144	
SO	SEQUENCE 144 AA; 15759 MW; 127828 CN;	

Query Match	49.8%;	Score 499;	DB 4;	Length 144;
Best Local Similarity	56.1%;	Pred. No. 3.32e-75;		
Matches	82;	Conservative	30;	Mismatches 24;
			Indels	9;
			Gaps	6;

Db	1	mavllallclatfpcslisgqqlkesgplvapsqslstctvsfsltg-ygvnvwirqp	59
		: : :	
Qy	1	MRVILLIMLITAFPG-ILSDVQLQESGPVVKPQSLSLTCVTGTSTSDHAWSIQRF	59
Db	60	pgkglewltgiwngstdynstlksrlititkdnksqvfikmnslqtddtaryycaasvi	119
Qy	60	PGNKLWEMVYSYSGITYNPISLKRISRTDTSKNQFFVLQLNSVTTGDTSTYICAR-SL	118
Db	120	yyvgrsedkyftldwaggtcvtves	144
		: : : :	
Qy	119	---ART-T---AMDYWGQGTSTVSS	137

RESULT	7	
ID	HV2G HUMAN	STANDARD:
		PRT: 117 AA

AC	P01825;
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE)
DT	21-JUL-1986 (REL. 01, CREAT SEQUENCE UPDATE)
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN V-II REGION (NEMM).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
RP	[1]
RP	SEQUENCE.
RM	77242302
RA	POLJAK R.J., NAKASHIMA Y., CHEN B.L., KONIGSBERG W.;
RRL	BIOCHEMISTRY 16:3412-3420(1977).
[2]	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RP	78066916
RA	SAUL F.A., AMZEL L.M., POLJAK R.J.;
RL	J. BIOL. CHEM. 253:585-597(1978).
CC	-I- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
DR	PIR; A02100; GIHMNM.
DR	PDB; 7FAB; 31-JAN-94.
KW	IMMUNOGLOBULIN V REGION; 3D-STRUCTURE.
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	NOD_TER 117 117
FT	STRAND 3 7
FT	STRAND 11 12
FT	TURN 14 15
FT	STRAND 18 25
FT	TURN 30 31
FT	STRAND 33 39
FT	TURN 41 42
FT	STRAND 46 51
FT	TURN 53 54
FT	STRAND 57 59
FT	HELIX 61 63
FT	TURN 64 66
FT	STRAND 67 72
FT	TURN 73 76
FT	STRAND 77 82
FT	HELIX 87 89
FT	STRAND 91 98
FT	STRAND 104 107
FT	STRAND 111 115
SQ	SEQUENCE 117 AA; 12790 MW; 79791 CN;

Query Match	48.0%; Score 481; DB 4; Length 117;
Best Local Similarity	54.6%; Pred. No. 1.40e-71;
Matches	65; Conservative 29; Mismatches 23; Indels 2; Gaps 2;
Ddb	1 qvqlseggplvrpsqtllktctvsqstfsendy-ytwvrqpbggrglwlgivfyfhgtedd 59 : : : : :           : : : : :   :         :   :   :   :
Oy	19 DWQLSEGPVLVKPQSLSLTCTVGVTSIDHAWSKIRPGPKLENNKMGIVISGITY 78 : : : : :           : : : : :   :         :   :       :
Ddb	60 ttplrervtmldtshknfslresvtadtavycarnli-agcidvwggselvtves 117 : : : : :           :   :       :           :   :       :
Oy	79 NPSLKSRISITRDTSKNQFFLQLNSVTGTSTYCYCARSLARTTAMDYWGQGSVTVS 137 : : : : :           :   :       :           :   :       :
RESULT	8
ID	HV02 XENLA STANDARD; PRT; 135 AA.
AC	P20957;
DT	01-FEB-1991 (REL. 17, CREATED)
DT	01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT	01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)

```
DE IG HEAVY CHAIN PRECURSOR V REGION (XIG14) (FRAGMENT).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RP SEQUENCE FROM N.A.
RM 88176921
RA SCHWAGER J., MIKORYAK C.A., STEINER L.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 85:2245-2249(1988).
DR EMBL; J03632; XLIGHB.
DR PIR; B31933; B31933.
DR HSSP; P01607; IFGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT NON TER      1       I
   SIGNAL        <1    18
   FT CHAIN     19    135
   FT CHAIN     19    135
   FT NON TER   135    135
SQ SEQUENCE     135 AA; 15080 MW; 104336 CN;
```

Query Match            48.0%; Score 481; DB 4; Length 135;  
Best Local Similarity 52.2%; Pred.No. 1.40e-71;  
Matches         71; Conservative 28; Mismatches 33; Indels 4; Gaps 4;

Dd      2 fiiiffifafpsccilsqt-lqespggtvkpxseisrltctvsgfclsyhm-hwirppg 59  
        :::: | | | ::| ::||| |||||:|||| |:||| ||  
Qy      4 LILLMLFATF-PG-IILSDVQLQESGPVLKVSQSLSLTCTVTGTSTDSHWASWRQPFG 61

Dd      60 kglwlgviatggstaiadslnrvttikdnkgkqvylgmngmekvtamycareyasg 119  
        : |||: | | : | : |||: | | | : | | : | | : | | : | | : | | | |

Qy      62 NKLEWMGYISYGITTPNPSLKRSRISTRTSRKNQFFLAQINSVTTGDTSTYYCARSLART 121  
        ||| ||| | ||| :

Dd      120 ynfdyvgaggtmvtvs 135

Qy      122 TAMDYNGOCTSIVTWS 137

RESULT	9	ID	HV21 HUMAN	STANDARD;	PRT;	146 AA.
AC		AC	P06331;			
DT		DT	01-JAN-1988	(REL. 06, CREATED)		
DT		DT	01-JAN-1988	(REL. 06, LAST SEQUENCE UPDATE)		
DT		DT	01-NOV-1990	(REL. 16, LAST ANNOTATION UPDATE)		
DE		DE	IG HEAVY CHAIN PRECURSOR V-II REGION (ARIH-77).			
OS		OS	HOMO SAPIENS (HUMAN).			
OC		OC	EUKARYOTA; METAZOA;			
OC		OC	EUTHERIA; PRIMATES.			
RN		RN	[1]			
RP		RP	SEQUENCE FROM N.A.			
RM		RM	85205332			
RA		RA	KUDO A., ISHIHARA T., NISHIMURA Y., WATANABE T.;			
RL		RL	GENE 33:181-189(1985).			
DR		DR	PIR; A02101; GI4HUH2.			
DR		DR	HSP; P01825; IFGV.			
KW		KW	IMMUNOGLOBULIN V REGION; SIGNAL.			
FT		FT	SIGNAL	1	19	
FT		FT	CHAIN	20	146	IG HEAVY CHAIN V-II REGION (ARIH-77).
FT		FT	DOMAIN	20	117	V SEGMENT.
FT		FT	DOMAIN	118	127	D SEGMENT.
FT		FT	DOMAIN	128	146	J SEGMENT.
FT		FT	DISULFID	42	115	BY SIMILARITY.
FT		FT	NON TER	146	146	
SQ		SQ	SEQUENCE	146 AA;	16228 MM;	127884 CN;
Query Match					46.8%;	Score 469; DB 4; Length 146;
Best Local Similarity					55.9%;	Pred. No. 3.59e-69;

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Matches 80; Conservative 24; Mismatches 28; Indels 11; Gaps 5;  
 Db 6 flllwclpdv-gvleqvlqagvlkpaetlsitcavfgsf-sgyvswirgppqr 63  
 :|||| : |||:||||: |||:||||:||||:| | : | ||||| ||  
 Qy 4 LILLM-LTAFPGILSDVQLQESGVLVWKPQSLSLCTCTVTGYSITSDHMSWIRQFPGN 62  
 64 glwigeinhegstnyktelkarvtlaidteknlfelklsevtadtaavyycargllrrg 123  
 ||||:| : ||| : |||:||||: ||||| | | :|||:||||: |||||:| |  
 Qy 63 KLEWGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTTYCARSLART- 121  
 Db 124 wmdvdyvvgmdvvgqgtvtvs 146  
 :|| :|||:|||||  
 Qy 122 -TAMDY-----WGQGTSTVTSS 137

RESULT 10  
 ID HV44 MOUSE STANDARD; PRT; 115 AA.  
 AC P01820;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (PJ14).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RM 81012133  
 RA SAKANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.;  
 RL NATURE 286:676-683(1980).  
 DR PIR: A02095; HWS14.  
 DR HSP: P01772; IFDL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 19  
 FT CHAIN 20 115 IG HEAVY CHAIN V REGION (PJ14).  
 FT NON TER 115 115  
 SQ SEQUENCE 115 AA; 12447 MW; 73384 CN;

Query Match 45.4%; Score 455; DB 4; Length 115;  
 Best Local Similarity 57.8%; Pred. No. 2,28e-66;  
 Matches 67; Conservative 23; Mismatches 24; Indels 2; Gaps 2;  
 Db 1 mavlllclvtfpccileqvlkpaetlsitcavfgsf-sgyvswirgppqr 59  
 :|||| : |||:||||: |||:||||:||||:| | : | ||||| ||  
 Qy 1 MRVLLMLTAFPG-ILSDVQLQESGVLVWKPQSLSLCTCTVTGYSITSDHMSWIRQF 59  
 60 pgkglewlgmivgdgtdynaalsrslskdsksqvflkmslqtdtdaryyca 115  
 |||:||||: | | :|||:||||:||||:| | :|||:| | :|||  
 Qy 60 PGNKLEWGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTTYCA 115

RESULT 11  
 ID HV45 MOUSE STANDARD; PRT; 116 AA.  
 AC P01821;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (MC101).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RM 82075900

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RA KATAOKA T., NIKAIKO T., MIYATA T., MORIWAKI K., HONJO T.;  
 RL J. BIOL. CHEM. 257:277-285(1982).  
 DR PIR: A02096; GIMS10.  
 DR HSP: P01772; IFDL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT SIGNAL 1 19  
 FT CHAIN 20 116 IG HEAVY CHAIN V REGION (MC101).  
 FT NON TER 116 116  
 SQ SEQUENCE 116 AA; 12593 MW; 75942 CN;

Query Match 44.1%; Score 442; DB 4; Length 116;  
 Best Local Similarity 53.8%; Pred. No. 8,99e-64;  
 Matches 63; Conservative 27; Mismatches 25; Indels 2; Gaps 2;  
 Db 1 mavlllclvtfpccileqvlkpaetlsitcavfgsf-sgyvswirgppqr 59  
 :|||| : |||:||||: |||:||||:||||:| | : | ||||| ||  
 Qy 1 MRVLLMLTAFPG-ILSDVQLQESGVLVWKPQSLSLCTCTVTGYSITSDHMSWIRQF 59  
 60 pgkglewlgmivgdgtdynaalsrslskdsksqvflkmslqtdtdaryyca 116  
 |||:||||: | | :|||:||||:||||:| | :|||:| | :|||  
 Qy 60 PGNKLEWGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTTYCAR 116

RESULT 12  
 ID HV01 XENLA STANDARD; PRT; 136 AA.  
 AC P20956;  
 DT 01-FEB-1991 (REL. 17, CREATED)  
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)  
 DE IG HEAVY CHAIN PRECURSOR V REGION (XIG8) (FRAGMENT).  
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RM 88176921  
 RA SCHWAGER J., MIKORYAK C.A., STEINER L.A.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 85:2245-2249(1988).  
 DR EXBL; M20484; XLIGHA.  
 DR PIR: A31933; A31933.  
 DR HSP: P01789; 2FGW.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT NON TER 1 1  
 FT SIGNAL <1 18  
 FT CHAIN 19 136 IG HEAVY CHAIN V REGION (XIG8).  
 FT NON TER 136 136  
 SQ SEQUENCE 136 AA; 15123 MW; 110289 CN;

Query Match 44.1%; Score 442; DB 4; Length 136;  
 Best Local Similarity 47.4%; Pred. No. 8,99e-64;  
 Matches 64; Conservative 33; Mismatches 35; Indels 3; Gaps 3;  
 Db 4 ifvifmffscileq-lqesgqvtvkpselritctvsgfcltvyv-wirgpprkt 61  
 :|||:| : |||:||||| |||||:||||:| | : ||||| |  
 Qy 4 LILLMLTAFPGILSDVQLQESGVLVWKPQSLSLCTCTVTGYSITSDHMSWIRQFPGN 63  
 62 lewigvrtgdstaidsalrvtitkdnkqkvylgmngmekvtdtamyctatlagtag 121  
 ||||:| : | : |||:||||:| | :|||:||||: |||:| | :|||  
 Qy 64 LEWGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTTYCARSLART 123  
 Db 122 yfhwgqgtmvtvs 136  
 : ||||| |||||  
 Qy 124 -MDYWGQGTSTVTSS 137

RESULT 13					
ID	HVZE HUMAN	STANDARD;	PRT;	121 AA.	
AC	P01878;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)				
DE	IG HEAVY CHAIN V-II REGION (HE).				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE.				
RM	70114712				
RA	CUNNINGHAM B.A., PFUJMM M.N., RUTISHAUSER U., EDELMAN G.M.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 64:997-1003(1969).				
CC	-I- THIS GAMMA-I CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.				
DR	PIR; A02093; GIHUHE.				
DR	HSSP; P01772; IFGV.				
KW	IMMUNOGLOBULIN V REGION.				
FT	MOD RES 1				
FT	NON_TER 121				
SQ	SEQUENCE 121 AA; 13483 MW; 85933 CN;				
 Query Match 43.7%; Score 438; DB 4; Length 121; Best Local Similarity 52.1%; Pred.No. 5,64e-63; Matches 63; Conservative 26; Mismatches 30; Indels 2; Gaps					
Dd	1 qvtlkengptlvkptetltlcttleglsittqdvavgwrqpggralawllwydddk 60 :   :       :::    ::  :                ::  :				
Qy	19 DVQLAESGVLKRFPSQSLSCTCTVTGYSTSD-HANSWRIQPFNGKLEWMGISY-SGIT 76 :   :       :::    ::  :                ::  :				
Dd	61 rfpselkerltvtrdstknqvltmtnpdvtatycvvhrrprtlaifdwgggtkvavs 120 :      :::    ::  : ::   :  : -              :				
Qy	77 TYNPSLKRSISITRDTSKNQFFIQINSVTGTSTYYCARSLARTANDYWGGTSVTVS 136 :      :::    ::  : ::   :  : -              :				
Dd	121 s 121				
Qy	137 s 137				
 RESULT 14					
ID	HV16 MOUSE	STANDARD;	PRT;	136 AA.	
AC	P01783;				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)				
DE	IG HEAVY CHAIN PRECURSOR V REGION (MOPC 21) (FRAGMENT).				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RM	81234548				
RA	BOTHELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,				
RA	BALTIMORE D.;				
RL	CELL 24:625-637(1981).				
RN	[2]				
RP	SEQUENCE OF 17-136.				
RM	71100368				
RA	ADETUGBO K., MILSTEIN C., SECHER D.S.;				
RL	NATURE 265:299-304(1977).				
DR	PIR; A02066; GIMS21.				
DR	HSSP; P01607; IFGV.				
KW	IMMUNOGLOBULIN V REGION; SIGNAL.				

FT	NON TER	I	I
FT	SIGNAL	<1	16
FT	CHAIN	17	136
FT	DOMAIN	115	119
FT	DOMAIN	120	136
FT	DISULFID	38	112
FT	NON TER	136	136
FT	CONFLICT	75	78
FT	CONFLICT	89	90
FT	CONFLICT	115	115
FT	CONFLICT	120	120
FT	CONFLICT	120	120
FT	SEQUENCE	136 AA;	15071 MW; 108615 CN;
Query Match		42.8%;	Score 429; DB 4; Length 136;
Best Local Similarity		47.1%;	Pred. No. 3.49e-61;
Matches	64;	Conservative	30; Mismatches 39; Indels 3; Gaps 3;
Db	2 lnlvflvlilkgqvcdqlvesggglvpqggrklscsaagftfss-fgmhwvrqapekg	60	
Qy	4 LILLWLTAFPGILSDVQLQESGVLVKQSLSLCTVTGVTSITSDHAWSWIRFPQGNK	63	
Db	61 lewvayissgstlhyadvtkgrftisrdbnphntlfqmtsrdsedamycarwgny	120	
Qy	64 LEHWGVIYSYGITT-YNPSIKRSISITRFSKNQFFLLQINSVTGTGSTYTCARSIA-RT	121	
Db	121 yamdyygggtstvtss	136	
Qy	122 TAMDYMGQGTSTVTSS	137	
RESULT 15			
ID	HVZF HUMAN STANDARD;	PRT;	129 AA.
AC	P01824;		
DT	21-JUL-1986 (REL. 01, CREATED)		
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)		
DE	21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)		
DE	IG HEAVY CHAIN V-II REGION (WAH).		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
CC	EUTHERIA; PRIMATES.		
RN	[1]		
RP	SEQUENCE.		
RM	82222235		
RA	TAKAHASHI N., TETAERT D., DEBUIRE B., LIN L.-C., PUTNAM F.W.;		
RL	PROC. NATL. ACAD. SCI. U.S.A. 79:2850-2854(1982).		
CC	-!- THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN.		
DR	PIR; A02099; D2HUWA.		
DR	HSP; P01607; IFGV.		
KW	IMMUNOGLOBULIN V REGION.		
FT	NON TER	129	129
FT	SEQUENCE	129 AA;	14117 MW; 95290 CN;
Query Match		42.4%;	Score 425; DB 4; Length 129;
Best Local Similarity		56.6%;	Pred. No. 2.17e-60;
Matches	56;	Conservative	23; Mismatches 19; Indels 1; Gaps 1;
Db	2 lqlqesqpvlkpsctslcticvsqgprrtgygwgrppqkglewgvvytsiy	61	
Qy	20 VQLQESCPVLKPSQSLSLCTVTGVTSIT-SDHAWSWIRFPQGNKLEWHMGVISYSGITY	78	
Db	62 npslrgrvtisdtsrnqfslnrlmsaadtamycarg	100	
Qy	79 NPSLKRSISITRFSKNQFFLLQINSVTGTGSTYTCARS	117	

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13

Search completed: Mon Jul 8 08:34:03 1996  
Job time : 32 secs.

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1

\*\*\*\*\*  
Release 2.1D John F. Collins, BioComputing Research Unit.  
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\*\*\*\*\*  
MPPerch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Mon Jul 8 08:34:49 1996; MasPar time 4.28 Seconds  
Tabular output not generated.  
\*\*\*\*\*  
Title: >US-08-137-117B-31  
Description: (1-137) from US08137117B.pep  
Perfect Score: 1002  
Sequence: 1 MRVLLILMLFTAFGILSDV.....LARTAMDYWGQTSVTVSS 137  
\*\*\*\*\*  
Scoring table: PAM 150  
Gap 11  
Searched: 70887 seqs, 8282111 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
\*\*\*\*\*  
Database: a-geneseq22  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14  
Statistics: Mean 30.530; Variance 155.534; scale 0.196  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.  
\*\*\*\*\*  
SUMMARIES  
Result No. Score Match Length DB ID Description Pred. No.  
1 1002 100.0 137 6 R28671 pPM-h1 protein produc 6.61e-72  
2 747 74.6 138 6 R29014 pUC-RVH-PM1f-4. 8.43e-51  
3 747 74.6 138 6 R29012 pUC-RVH-PM1f. 8.43e-51  
4 726 72.5 240 7 R34510 Fv(TU27). 4.52e-49  
5 721 72.0 130 6 R33308 MaE13 heavy chain. 1.16e-48  
6 704 70.3 126 5 R24722 Sequence encoded by t 2.91e-47  
7 686 68.5 122 5 R24721 Sequence of a chimeri 8.77e-46  
8 664 66.3 114 9 R48617 Sequence of the monoc 5.60e-44  
9 664 66.3 117 2 R07318 VH domain of antibody 5.60e-44  
10 656 65.5 225 12 R63118 VH chain of 58.2 a 2.54e-43  
11 615 61.4 134 6 R33306 MaE11 heavy chain. 5.76e-40  
12 611 61.0 113 7 R38608 HYH heavy chain. 1.22e-39  
\*\*\*\*\*

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13 606 60.5 137 6 R33310 MaE15 heavy chain. 3.13e-39  
14 596 59.5 909 10 R50092 Humanised anti-CEA sF 2.06e-38  
15 589 58.8 240 1 P80157 Biosynthetic antibody 7.66e-38  
16 582 58.1 134 6 R33345 Sequence of the varia 2.85e-37  
17 576 57.5 134 9 R48613 Sequence of the monoc 8.80e-37  
18 572 57.1 117 8 R40953 Human germ-line gene 1.86e-36  
19 572 57.1 119 6 R30143 MAB GAH variable regi 1.86e-36  
20 569 56.8 121 13 R65171 Murine NM-01 variable 3.27e-36  
21 569 56.8 121 9 R48614 Sequence of the monoc 3.27e-36  
22 567 56.6 121 13 R65173 Region for producing 4.76e-36  
23 545 54.4 118 5 R29701 431/26 VH hum. 2.94e-34  
24 542 54.1 120 9 R48621 Sequence of the human 5.16e-34  
25 534 53.3 117 12 R66320 Human immunoglobulin 2.30e-33  
26 533 53.2 142 7 R41285 F105 rearranged varia 2.78e-33  
27 533 53.2 144 10 R53344 NEMM human Ab H chain 2.78e-33  
28 531 53.0 135 2 P70991 Sequence of the heavy 4.04e-33  
29 529 52.8 117 7 R38669 Ab26. 5.87e-33  
30 527 52.6 141 6 R31948 Anti-CD4 VH peptide. 8.53e-33  
31 526 52.5 118 12 R66322 Human immunoglobulin 1.03e-32  
32 523 52.2 116 12 R66346 Human immunoglobulin 1.80e-32  
33 523 52.2 116 7 R42689 Vh 71-4. 1.80e-32  
34 523 52.2 118 12 R66348 Human immunoglobulin 1.80e-32  
35 520 51.9 124 2 R12266 Anti-human Rhd PAG-1 3.15e-32  
36 516 51.5 220 12 R74782 Heavy chain of 59.1 a 6.66e-32  
37 513 51.2 122 6 R30145 MAB 1-3-1 variable re 1.17e-31  
38 511 51.0 470 4 R22757 Reshaped CAMPATH-1 an 1.69e-31  
39 509 50.8 183 6 R32128 Anti-IL2R-alpha antib 2.46e-31  
40 509 50.8 183 3 R15326 IL-2 chimeric antibod 2.46e-31  
41 507 50.6 111 4 R22574 Heavy chain VH14.1 fr 3.57e-31  
42 507 50.6 114 12 R62919 Human cytomegalovirus 3.57e-31  
43 507 50.6 120 10 R54929 Fc receptor humanized 3.57e-31  
44 506 50.5 144 1 P80892 V region of H chain o 4.30e-31  
45 504 50.3 242 2 R06483 18-2-3-/TRV59. 6.25e-31

ALIGNMENTS

RESULT 1  
ID R28671 standard; Protein; 137 AA.  
AC R28671;  
DT 30-MAR-1993 (first entry)  
DE pPM-h1 protein product.  
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
KW heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;  
KW plasmid; pPM-k3; pPM-h1.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..18  
FT /note= "Signal peptide"  
FT Protein 19..137  
FT /note= "Mature peptide"  
PN W09219759-A.  
PD 12-NOV-1992.  
PF 24-APR-1992; J00544.  
PR 25-APR-1991; JP-095476.  
PR 19-FEB-1992; JP-032084.  
PA (CHUS ) CHUGAI SEIYAKU KK.  
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
DR WPI; 92-398882/48.  
DR N-PSDB; Q30756.  
PT Reconstituted human antibody to human interleukin-6 receptor -  
PT has low antigenicity and contains mouse V-region complementarity  
PT determining regions  
PS Disclosure; Page 122-123; 207pp; Japanese.



The sequences given in R28670-71 were encoded by plasmids which were used in example 1 to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PM1 which contained the plasmids pBW-K3 and pBW-h1. Sequence 137 AA;

	Query Match	100.0%;	Score 1002;	DB 6;	Length 137;
	Best Local Similarity	100.0%;	Pred. No. 6,61e-72;	Mismatches 0;	Gaps 0;
	Matches 137;	Conservative			
Db	1	mrvlllwlftapgilvedqlgesgplvlpksqslstctvtgytsdhwswirfp	60		
Qy	1	mrvlllwlwtapgilssdqvlqesgpvlvpkqsllacttvgysitshawsirfep	60		
Db	61	gnklewmgyisyggittynpsalrkitrdtsknqfflnsvttgdtsyycarslar	120		
Qy	61	gnklewmgyisyggittynpsalkrsisitrdsnkqfflqnlsvttgttyycarslar	120		
Db	121	ttaamywagqtstvtes	137		
Qy	121	TTAAMDYWGQTSTVTSS	137		

RESULT	ID	Location/Qualifiers
2	R29014 standard; Protein; 138 AA.	
AC	R29014;	
DE	30-MAR-1993 (first entry)	
DT	pUC-RVH-PW1-4.	
DE	Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;	
KW	complementarity determining region; mouse; monoclonal; hybridoma;	
KW	plasmid; polymerase chain reaction; amplify.	
KW	Synthetic.	
OS		
FT	Key	
FT	Peptide	1..19
FT	/note= "Leader peptide"	20..49
FT	Region	
FT	/label= FR1	50..55
FT	Region	
FT	/label= CDR1	56..69
FT	Region	
FT	/label= FR2	70..85
FT	Region	
FT	/label= CDR2	86..117
FT	Region	
FT	/label= FR3	118..127
FT	Region	
FT	/label= CDR3	128..138
FT	Region	
FT	/label= FR4	
PN	W09219759-A.	
PD	12-NOV-1992.	
PP	24-APR-1992; J00544.	
PR	25-APR-1991; JP-095476.	
PR	19-FEB-1992; JP-032084.	
PR	(CHUS ) CHUGAI SEIYAKU KK.	
PA	Bendig MM, Jones ST, Saldanha JW, Sato K, Teuchiya M;	
PI	WPI; 92-398882/48.	
DR	N-PSDB; Q31365.	
PT	Reconstituted human antibody to human interleukin-6 receptor -	
PT	has low antigenicity and contains mouse V-region complementarity	
PT	determining regions	
PT	PS Disclosure: Page 142-3; 207top; Japanese.	

CC The sequences given in R20012-15 are portions of monoclonal antibodies  
CC which were encoded by plasmids derived from mouse hybridomas. The DNA  
CC encoding complementarity determining regions (CDR's) was isolated by  
CC polymerase chain reaction. These antibodies recognise human  
CC interleukin-6 receptor (II-6R). The mouse hybridoma cells were  
CC transformed with the plasmids encoding these genes which caused the  
CC secretion of these antibodies from the hybridoma cells.  
SQ Sequence 138 AA;

	Query Match	74.6%;	Score 747;	DB 6;	Length 138;
	Best Local Similarity	75.9%;	Pred. No.	8.43e-51;	
	Matches	101;	Conservative	19;	Mismatches 13; Indels 0; Gaps 0;
D <sub>b</sub>	6	ilflvatatghsqvqlgsgqglvrpsqtlsitctvsygsitedshawswwirppgrgl	65		
	:	: :	: : :	: : :	: : :
	:	: :	: : :	: : :	: : :
Q <sub>y</sub>	5	ILLILFTAFPGILLSDVQLQGEGCPVLKPKSQSLSTCTVTCYGSITSDHANSWIRQPFGNKL	64		
D <sub>b</sub>	66	ewiqvisysgittynpsiksrtvmldtsknqfslrlssvtadtavvycaarslarttam	125		
	:	: : :	: : :	: : :	: : :
Q <sub>y</sub>	65	EWMGYISYGITTYPNSIKSRISITRDTSKNQFGLINSVTTGDTSTYYCARSLARTTAM	124		
D <sub>b</sub>	126	dyywgqgslvtvss	138		
	:	: : :	: : :	: : :	: : :
O <sub>v</sub>	125	DYWGCGTSVTWSS	137		

RESULT	3	
ID	R29012 standard; Protein; 138 AA.	
AC	R29012;	
DE	30-MAR-1993 (first entry)	
DT	pUC-RVh-PM1f.	
DE	Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;	
KW	complementarity determining region; mouse; monoclonal; hydridoma;	
KW	plasmid; polymerase chain reaction; amplify.	
OS	Synthetic.	
Key	Location/Qualifiers	
FT	Peptide	1..19
FT	/note= "Leader peptide"	
FT	Region	20..49
FT	/label= FR1	
FT	Region	50..55
FT	/label= CDR1	
FT	Region	56..69
FT	/label= FR2	
FT	Region	70..85
FT	/label= CDR2	
FT	Region	86..117
FT	/label= FR3	
FT	Region	118..127
FT	/label= CDR3	
FT	Region	128..138
FT	/label= FR4	
PN	W09219759-A.	
PD	12-NOV-1992.	J00544.
PF	24-APR-1992;	
PR	25-APR-1991; JP-095476.	
PR	19-FEB-1992; JP-032084.	
PA	(CHUS ) CHUGAI SEIYAKU KK.	
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Tauchiya M;	
DR	WPI; 92-398882/48.	
DR	N-PSDB: Q31360.	
PT	Reconstituted human antibody to human interleukin-6 receptor -	
PT	has low antigenicity and contains mouse V-region complementarity	
PT	determining regions	



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FT Region 102...113  
 FT /label= CDR 3  
 PN EP-491351-A.  
 PD 24-JUN-1992.  
 PF 17-DEC-1991; 121591.  
 PR 18-DEC-1990; JP-413829.  
 PA 11-NOV-1991; JP-294464.  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 PI Iwasa S, Taka H, Watanabe T, Tada H;  
 PI WPI; 92-209528/26.  
 DR N-PSDP; Q25667.  
 DR Chimeric monoclonal antibodies - contain anti-human fibrin  
 PT antibody light and heavy chain variable and constant for treating  
 PT thrombotic conditions e.g. myocardial infarction  
 PS Example; Figure 15; 87pp; English.  
 CC Poly(A)+ RNA was prep'd. from mouse anti-urokinase  
 CC antibody-producing hybridoma UK1-3 cells. Using this poly(A) RNA as  
 CC a template, an anti-urokinase antibody VK cDNA was amplified with  
 CC the mC-kappa primer as primer for first strand synthesis, and the  
 CC 3'mV-kappa and 5'mV-kappa primers as primers for the PCR. The  
 CC amplified fragment was restriction digested and ligated into a  
 CC restriction fragment of pTB1423 to give an anti-urokinase antibody  
 CC VK cDNA contg. plasmid pTB1456. The sequence of this plasmid is  
 CC given in Q25667. The cDNA is a functional VK gene. The sequence of  
 CC the primer (mC-gamma-1) is given in Q25689.  
 SQ Sequence 126 AA;

Query Match 70.3%; Score 704; DB 5; Length 126;  
 Best Local Similarity 81.0%; Pred. No. 2.91e-47;  
 Matches 98; Conservative 10; Mismatches 11; Indels 2; Gaps 2;  
 Db 4 evqlvespgqlvkpsqslctctvgtysitedatycarlqgfdagdyfdywgqgtttvs 123  
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||  
 QY 19 DVQLQESGPVLVWPKPSQSLSLCTCTVGTGYSITSDHAWSWIRQFPGNKLEWNGYISYGITY 78  
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||  
 Db 64 npslksrisitrdtnnqfflqlnsvtsedatycarlqgfdagdyfdywgqgtttvs 123  
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||  
 QY 79 NPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCAR-S-LARTTAMDYWGQGTSTVTS 136

Db 124 s 124  
 QY 137 s 137  
 RESULT 7  
 ID R24721 standard; Protein; 122 AA.  
 AC R24721;  
 DT 28-DEC-1992 (first entry)  
 DE Sequence of a chimeric urokinase-recognising antibody heavy chain  
 DE variable region contg. complementarity determining regions (CDRs)  
 DE J, K and L.  
 KW Chimeric monoclonal antibody; anti-urokinase antibody;  
 KW antithrombotic agent; myocardial infarction therapy.  
 OS Synthetic.  
 FS Key Location/Qualifiers  
 FT Region 31...36  
 FT /label= CDR J  
 FT Region 51..66  
 FT /label= CDR K  
 FT Region 99..110  
 FT /label= CDR L  
 PN EP-491351-A.  
 PD 24-JUN-1992.  
 PF 17-DEC-1991; 121591.

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PR 18-DEC-1990; JP-413829.  
 PR 11-NOV-1991; JP-294464.  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 PI Iwasa S, Taka H, Watanabe T, Tada H;  
 PI WPI; 92-209528/26.  
 PR Chimeric monoclonal antibodies - contain anti-human fibrin  
 PT antibody light and heavy chain variable and constant for treating  
 PT thrombotic conditions e.g. myocardial infarction  
 PS Disclosure; Page 10; 87pp; English.  
 CC The inventors claim a chimeric monoclonal antibody which contains a  
 CC urokinase-recognising antibody heavy chain variable region contg. at  
 CC least one of the polypeptide chains J, K and L (R24717, R24718, R24719)  
 CC and a human antibody heavy chain constant region. A pref'd. chimeric  
 CC monoclonal antibody contains all three complementarity determining  
 CC regions. The chimeric Abs can be used both in vivo and in vitro  
 CC and, since they have very low immunogenicity as compared with mouse  
 CC Abs, they can be administered to humans for diagnostic and  
 CC therapeutic purposes. They are also more stable and show a longer  
 CC half-life in the blood as compared with the original mouse Abs.  
 SQ Sequence 122 AA;

Query Match 68.5%; Score 686; DB 5; Length 122;  
 Best Local Similarity 80.2%; Pred. No. 8.77e-46;  
 Matches 97; Conservative 10; Mismatches 11; Indels 3; Gaps 3;  
 Db 1 evqlvespgqlvkpsqslctctvgtysitedatycarlqgfdagdyfdywgqgtttvs 59  
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||  
 QY 19 DVQLQESGPVLVWPKPSQSLSLCTCTVGTGYSITSDHAWSWIRQFPGNKLEWNGYISYGITY 78  
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||  
 Db 60 npslksrisitrdtnnqfflqlnsvtsedatycarlqgfdagdyfdywgqgtttvs 119  
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||  
 QY 79 NPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCAR-S-LARTTAMDYWGQGTSTVTS 136  
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||  
 Db 120 s 120  
 QY 137 s 137

RESULT 8  
 ID R48617 standard; Protein; 114 AA.  
 AC R48617;  
 DT 03-SEP-1994 (first entry)  
 DE Sequence of the monoclonal antibody BAT123 heavy chain  
 DE variable region.  
 KW Epitope; monoclonal antibody; BAT123; variable heavy.  
 OS Synthetic.  
 PN W09404574-A.  
 PD 03-MAR-1994.  
 PF 24-AUG-1993; U07967.  
 PR 24-AUG-1992; WO-007111.  
 PR 22-APR-1993; US-039457.  
 PA (NISP ) NISSIN SHOKUIN KAISHA LTD.  
 PI Ohno T;  
 DR WPI; 94-083117/10.  
 PT New humanised antibody specific for epitope on HIV-1 gp 120 -  
 PT able to neutralise infection of HG cells, also nucleic acid  
 PT encoding it, useful for passive immunisation to treat or prevent  
 PT HIV-1 infection  
 PS Example; Page 46-47; 91pp; English.  
 CC GPCR is a portion of HIV-1 gp120 or gp160 protein. Monoclonal  
 CC antibodies (MAbs) that react with this and which have the capacity  
 CC to neutralise the infection of H9 cells in culture by live HIV-1  
 CC strains MN and IIIB are claimed. Specifically illustrating the  
 CC invention are the murine MAbs (designated NM-01) produced by

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CC hubridoma cell line HB 10726 which is deposited under ATCC No. HB 10726. The DNA sequences of the variable regions of the heavy and light chains of Mab NM-01 were cloned by PCR using cDNA generated from hybridoma HB 10726 cytoplasmic RNA as template. The DNA was then sequenced. The DNA and deduced AA sequences are given in CC Q56685/R48613; Q56686/R48615. Resequencing the variable regions of Mab NM-01 resulted in the sequences set out in Q56687/R48614 CC and Q56688/R48616. The heavy chain variable region of NM-01 CC differs from that of the Mab BA123, as reported in Liou et al., CC by 46 AAs out of a total of 120. The light chain variable regions CC of these two Abs differ by 23 AAs. Significantly, the three CDRs CC in the heavy chain (V-H) of the NM-01 molecule are about 41 to 90% CC different in sequence from those of BA123, while the sequences of CC the three CDRs in the light chain (V-L) vary by about 29-47% CC compared to NM-01.

SQ Sequence 114 AA;

Query Match 66.3%; Score 664; DB 9; Length 114;  
Best Local Similarity 82.4%; Pred. No. 5,60e-44;  
Matches 98; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

Db 1 evqlqesgdlvlpqsglslelctvtgysitdsydwawwlrqfpgnklemgysygetty 60  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
Qy 19 DVQLQESGVLVLPKPSQSLSLTCTVTCYSITSDHAWSWIRQPPGNKLEMGYISYSGITTY 78

Db 61 npslkerisrtdsknflqlsvsteedtatyccary---sfg-d-wgqgtlvtvsa 114  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
Qy 79 NPSLKSRSISITRDTSKNQFFLQLNSVTTCGDTSTYCARSLARTTANDYWGQGTSTVTSS 137

RESULT 9

ID R07318 standard; protein; 117 AA.

AC R07318;  
DT 22-JAN-1991 (first entry)  
DE VH domain of antibody B against tumour-associated antigens.  
KW Tumour-associated antigen; murine monoclonal antibody B;  
KW gastrointestinal carcinoma; ovary; pulmonary adenocarcinoma;  
KW diagnosis.  
OS Mus musculus.  
PN EP-388914-A.  
PD 26-SEP-1990.  
PF 21-MAR-1990; 105322.  
PR 24-MAR-1989; DE-909799.  
PA (BEHW ) BEHRINGERWERKE AG.  
PI Bosslet K, Seemann G, Sedlacek HH;  
DR WPI; 90-291873/39.  
DR N-PSDB; Q07318.  
PT Monoclonal antibodies to tumour associated antigens - used for  
PT diagnosis of malignant tumours etc.  
PS Disclosure; Page 12; 18pp; German.  
CC Antibody B is produced as described in EP-141079 and binds to cells  
CC almost all gastrointestinal carcinomas and to certain ovary  
CC carcinomas and pulmonary adenocarcinomas.  
CC They are useful in tumour diagnosis and therapy.  
CC See also Q06215 for VK of Mab B, Q07312-13 for Mab A and Q06227-30  
CC for Mab C and D.  
SQ Sequence 117 AA;

Query Match 66.3%; Score 664; DB 2; Length 117;  
Best Local Similarity 82.1%; Pred. No. 5,60e-44;  
Matches 96; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

Db 1 lqesgdlvlpqsglslelctvtgysitdsydwawwlrqfpgnklemgysygetty 60  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

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10

Qy 22 LQESGVLVLPKPSQSLSLTCTVTCYSITSDHAWSWIRQPPGNKLEMGYISYSGITTYPS 81

Db 61 lkerisrtdsknflqlnsrvttedatyccaredydhwyfdwaggtvtvss 117  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
Qy 82 LKRSISITRDTSKNQFFLQLNSVTTCGDTSTYTCAR-SLARTTANDYWGQGTSTVTSS 137

RESULT 10

ID R63118 standard; peptide; 225 AA.

AC R63118;  
DT 26-JUN-1995 (first entry)  
DE Heavy chain of 58.2 an anti-HIV antibody.  
KW Identifying compounds; anti-HIV antibodies; HIV treatment;  
KW peptide AS; antibody 58.2.  
OS Homo sapiens.

FH Key Location/Qualifiers  
FT Modified site 160  
FT /label= OTHER  
FT /note= "CPR no further definition"  
FT Modified site 162  
FT /label= OTHER  
FT /note= "CPR no further definition"  
FT Modified site 201  
FT /label= OTHER  
FT /note= "CPR no further definition"  
PN W09418232-A.  
PD 18-AUG-1994.  
PF 09-FEB-1994; U01458.  
PR 12-FEB-1993; U017485.  
PA (REPK ) REPLIGEN CORP.  
PA (SCRI ) SCRIPPS RES INST.  
PI Profy AT, Wilson IA;  
DR WPI; 94-332662/41.  
PT Identifying cpds. which elicit, or bind to, anti-HIV antibodies -  
PT and new antibodies which neutralise a broad range of HIV strains  
PS Disclosure; Page 50; 137pp; English.  
CC R63118 describes the amino acid sequence of the heavy chain of  
CC 58.2 an anti-HIV antibody (Ab), it was used in the development of  
CC the peptide AS (R63119). This peptide can bind to anti-HIV Abs or  
CC elicit new Abs effective against a broad range of HIV strains,  
CC that can be used in the treatment of HIV infection.  
SQ Sequence 225 AA;

Query Match 65.5%; Score 656; DB 12; Length 225;  
Best Local Similarity 78.6%; Pred. No. 2,54e-43;  
Matches 99; Conservative 10; Mismatches 10; Indels 7; Gaps 3;

Db 1 dvqlqesgdlvlpqsglslelctvtgysitdsydwawwlrqfpgnklemgysygetty 60  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
Qy 19 DVQLQESGVLVLPKPSQSLSLTCTVTCYSITSDHAWSWIRQPPGNKLEMGYISYSGITTY 78

Db 61 npslkerisrtdsknflqlnsrvttedatyccareampygnqayyvamdvgggt 120  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
Qy 79 NPSLKSRSISITRDTSKNQFFLQLNSVTTCGDTSTYTCAR-SLA---RTT-AMDYWGQGT 131  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
Db 121 tvttvss 126  
:|||||  
Qy 132 SVTVSS 137

RESULT 11  
ID R33306 standard; protein; 134 AA.  
AC R33306;  
DT 05-JUL-1993 (first entry)

CC complex) (R38602-03 and R38609-10, respectively), NEMM [Ig Fab' NEMM]  
CC (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and  
CC R38612, respectively) may be used to determine an alignment from which  
CC appropriate changes may be made.  
CC Unlike other methods of humanisation, which advocate the  
CC replacement of entire antibody framework regions with those of human  
CC antibodies, this method involves only the introduction of human  
CC residues into those positions not critical for antigen binding.  
CC This ensures that the binding properties of the modified antibody  
CC are not diminished.  
SQ Sequence 113 AA;

Query Match	61.0%;	Score 611;	DB 7;	Length 113;
Best Local Similarity	77.3%;	Pred. No. 1.22e-39;		
Matches 92;	Conservative 12;	Mismatches 9;	Indels 6;	Gaps 5;
Db	1	dvlqesgplvpqcdlsclscvtgdsitdy-wswirkfgpnrlaymgyvsgstyy	59	
Qy	19	DVLQESGFLVLPQSLSLTCTVTGYISLTDHAWSIQFPKNLEWMCYISYSGITTY	78	
Db	60	npalkerisirdtstknqydlinsvttedatyyca-n--wd-g-dyqggtstvtva	113	
Qy	79	NPSLKRSIRISPTSKNOFFQLNLSVTTGDTSTYTCARSILRTATMDYVGQSTVTSV	137	

RESULT	13
ID	R33310 standard; Protein; 137 AA.
AC	R33310;
AD	05-JUL-1993 (first entry)
DT	DE MAEL3 heavy chain.
DE	KW Antibody; high affinity; FcER; IgE receptor; histamine; mast cell; murine; MAEL1; MAEL3; MAEL5; MAEL6; MAEL7; MAEL8; MAEL9; MAEL10; MAEL11; MAEL12; MAEL13; MAEL14; MAEL15; MAEL16; MAEL17; MAEL18; MAEL19; MAEL20; MAEL21; MAEL22; MAEL23; MAEL24; MAEL25; MAEL26; MAEL27; MAEL28; MAEL29; MAEL30; MAEL31; MAEL32; MAEL33; MAEL34; MAEL35; MAEL36; MAEL37; MAEL38; MAEL39; MAEL40; MAEL41; MAEL42; MAEL43; MAEL44; MAEL45; MAEL46; MAEL47; MAEL48; MAEL49; MAEL50; MAEL51; MAEL52; MAEL53; MAEL54; MAEL55; MAEL56; MAEL57; MAEL58; MAEL59; MAEL60; MAEL61; MAEL62; MAEL63; MAEL64; MAEL65; MAEL66; MAEL67; MAEL68; MAEL69; MAEL70; MAEL71; MAEL72; MAEL73; MAEL74; MAEL75; MAEL76; MAEL77; MAEL78; MAEL79; MAEL80; MAEL81; MAEL82; MAEL83; MAEL84; MAEL85; MAEL86; MAEL87; MAEL88; MAEL89; MAEL90; MAEL91; MAEL92; MAEL93; MAEL94; MAEL95; MAEL96; MAEL97; MAEL98; MAEL99; MAEL100; MAEL101; MAEL102; MAEL103; MAEL104; MAEL105; MAEL106; MAEL107; MAEL108; MAEL109; MAEL110; MAEL111; MAEL112; MAEL113; MAEL114; MAEL115; MAEL116; 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MAEL565; MAEL566; MAEL567; MAEL568; MAEL569; MAEL570; MAEL571; MAEL572; MAEL573; MAEL574; MAEL575; MAEL576; MAEL577; MAEL578; MAEL579; MAEL580; MAEL581; MAEL582; MAEL583; MAEL584; MAEL585; MAEL586; MAEL587; MAEL588; MAEL589; MAEL590; MAEL591; MAEL592; MAEL593; MAEL594; MAEL595; MAEL596; MAEL597; MAEL598; MAEL599; MAEL600; MAEL601; MAEL602; MAEL603; MAEL604; MAEL605; MAEL606; MAEL607; MAEL608; MAEL609; MAEL610; MAEL611; MAEL612; MAEL613; MAEL614; MAEL615; MAEL616; MAEL617; MAEL618; MAEL619; MAEL620; MAEL621; MAEL622; MAEL623; MAEL624; MAEL625; MAEL626; MAEL627; MAEL628; MAEL629; MAEL630; MAEL631; MAEL632; MAEL633; MAEL634; MAEL635; MAEL636; MAEL637; MAEL638; MAEL639; MAEL640; MAEL641; MAEL642; MAEL643; MAEL644; MAEL645; MAEL646; MAEL647; MAEL648; MAEL649; MAEL650; MAEL651; MAEL652; MAEL653; MAEL654; MAEL655; MAEL656; MAEL657; MAEL658; MAEL659; MAEL660; MAEL661; MAEL662; MAEL663; MAEL664; MAEL665; MAEL666; MAEL667; MAEL668; MAEL669; MAEL670; MAEL671; MAEL672;

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met, 53-094007/11.  
Poly peptide (e) binding to specific Fc epsilon receptors - act as  
Ige antagonists; useful for treating and preventing Ige-mediated  
disorders e.g. allergies  
Disclosure; Fig 2; 113pp; English.  
Antibodies capable of binding FcE1-bound Ige but which are  
substantially incapable of binding FcE1-bound Ige or inducing  
histamine release from mast cells or basophils, comprise a human  
Kabat CDR domain into which has been substituted a positionally  
analogous residue from a Kabat CDR domain of the murine anti-huIge  
antibodies MAE11, MAE13, MAE15 or MAE17.  
Sequence 137 AA;

	Query Match	60.5%;	Score 606;	DB 6;	Length 137;		
	Best local Similarity	76.6%;	Pred. No. 3.13e-39;				
	Matches	95;	Conservative	5; Mismatches	19; Indels	5; Gaps	2;
Db	1	dvdqcesepdlvtpsgslcttvtgysitgnynrhwiqfpgnklewmyihyagstny	60				
Qy	19	DVQLQSGEVLKVPESLSLTCTVTGYSITSDHAWSIROFFGNKLWNGYISYGITY	78				
Db	61	npslkrriisiddtsknqfflnsvttedatvcargsiyygsryrvfdwgaagtiv	120				



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 \* W E L C O M E T O T H E \*  
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=> s human interleukin 6 receptor?

133546 HUMAN  
 2317 INTERLEUKIN  
 1835874 6

23249 RECEPTOR?

L1 3 HUMAN INTERLEUKIN 6 RECEPTOR?  
 (HUMAN(W) INTERLEUKIN(W) 6(W) RECEPTOR?)

=> d 1-3 bib ab clm

US PAT NO: 5,447,851 [IMAGE AVAILABLE] L1: 1 of 3  
 DATE ISSUED: Sep. 5, 1995  
 TITLE: DNA encoding a chimeric polypeptide comprising the  
 extracellular domain of TNF receptor fused to IgG,  
 vectors, and host cells  
 INVENTOR: Bruce A. Beutler, Dallas, TX  
 Karsten Peppel, Dallas, TX  
 David F. Crawford, Irving, TX  
 ASSIGNEE: Board of Regents, The University of Texas System, Austin,  
 TX (U.S. corp.)  
 APPL-NO: 07/862,495  
 DATE FILED: Apr. 2, 1992  
 ART-UNIT: 182  
 PRIM-EXMR: Garnette D. Draper  
 ASST-EXMR: K. Cochrane Carlson  
 LEGAL-REP: Arnold, White & Durkee

US PAT NO: 5,447,851 [IMAGE AVAILABLE] L1: 1 of 3

# ABSTRACT:

The invention relates generally to DNA sequences encoding chimeric polypeptides comprising extracellular portions of cytokine receptor polypeptides attached to a sequence encoding portions of IgG polypeptides. The invention relates generally, as well, to DNA sequences encoding chimeric polypeptides comprising extracellular portions of cytokine receptor polypeptides attached through oligomers encoding specifically cleavable peptide linkers to a sequence encoding portions of IgG heavy chain polypeptides. More specifically, the invention relates to a construction in which a cDNA sequence encoding the extracellular domain of the human 55 kD TNF receptor is attached through an oligomer encoding a thrombin-sensitive peptide linker to a sequence encoding the F.sub.c portion and hinge region of a mouse IgG1 heavy chain. The invention relates as well to uses of the chimeric polypeptide, including: use as a reagent for the antagonism and assay of TNF and lymphotoxin from diverse species; use as a means of determining the mechanism by which TNF, or analogs thereof, interacts with the TNF receptor; use as an antitumor reagent, particularly against placental tumors; and, use as a reagent capable of controlling birth.

# CLAIMS:



CLMS(1)

What is claimed is:

1. An isolated DNA segment having a sequence encoding a chimeric polypeptide comprising the extracellular domain of a TNF receptor polypeptide functionally attached to a Fc portion and hinge region of an IgG heavy chain polypeptide.

CLMS(2)

2. The isolated DNA segment of claim 1, where the TNF receptor polypeptide is a human TNF receptor polypeptide.

CLMS(3)

3. The isolated DNA segment of claim 1, where the IgG heavy chain polypeptide is a mouse IgG polypeptide.

CLMS(4)

4. The isolated DNA segment of claim 1, further incorporating a DNA segment encoding a specifically cleavable linker peptide functionally interposed between the TNF receptor polypeptide and the Fc portion.

CLMS(5)

5. The isolated DNA segment of claim 4, where the specifically cleavable linker peptide comprises a thrombin-sensitive linker peptide.

CLMS(6)

6. A recombinant vector incorporating a DNA segment as defined by claim 1.

CLMS(7)

7. The recombinant vector of claim 6, where the TNF receptor polypeptide is a human TNF receptor polypeptide.

CLMS(8)

8. The vector of claim 6, where the IgG heavy chain polypeptide is a mouse IgG polypeptide.

CLMS(9)

9. The vector of claim 6, further incorporating a specifically cleavable linker peptide functionally interposed between the extracellular domain of the TNF receptor polypeptide and the Fc portion.

CLMS(10)

10. The vector of claim 9, where the specifically cleavable linker peptide comprises a thrombin-sensitive linker peptide.

CLMS(11)

11. The vector of claim 6, where the chimeric polypeptide encoding sequence is positioned adjacent to and under the control of an effective promoter.

CLMS(12)

12. The vector of claim 11, where the promoter comprises a prokaryotic promoter, the vector being adapted for expression in a prokaryotic host.

CLMS(13)

13. The vector of claim 11, where the promoter comprises a eukaryotic promoter, the vector being adapted for expression in a eukaryotic host, and the vector further includes a polyadenylation signal position 3' of the carboxy-terminal amino acid, and within a transcriptional unit of the encoding polypeptide.

CLMS(14)

14. The vector of claim 13, where the eukaryotic promoter comprises a cytomegalovirus promoter.

CLMS(15)

15. The recombinant host cell which incorporated an isolated DNA segment in accordance with claim 1.

CLMS(16)

16. The recombinant host cell of claim 15, further defined as a eukaryotic host cell.

CLMS(17)

17. The recombinant host cell of claim 16, further defined as a CHO cell.

CLMS(18)

18. The recombinant host cell of claim 15, further defined as a prokaryotic host cell.

CLMS(19)

19. The recombinant host cells of claim 15 where the DNA segment encoding a chimeric polypeptide is under the transcriptional control of regulatory signals functional in the recombinant host cell which regulatory signals appropriately control the expression of the chimeric polypeptide in a manner to allow all necessary transcriptional and post transcriptional modification.

CLMS(20)

20. A method of producing a chimeric polypeptide comprising the extracellular domain of the TNF receptor polypeptide functionally attached to a Fc portion and hinge region of an IgG heavy chain polypeptide, the method comprising:

(a) producing a recombinant host cell according to claim 5, such cell

- being capable of expressing the polypeptide;
- (b) culturing the host cell under conditions appropriate for expressing the polypeptide; and
- (c) recovering the chimetic polypeptide.

CLMS (21)

21. The method of claim 20, where additional steps comprise:
- (a) cleaving the polypeptide at the specifically cleavable linker peptide; and
  - (b) recovering the polypeptide comprising an extracellular domain of the TNF receptor polypeptide.

CLMS (22)

22. The method of claim 20 wherein the host cell is a eukaryotic cell.

CLMS (23)

23. The method of claim 22 wherein the eukaryotic cell is a CHO cell.

CLMS (24)

24. The method of claim 22 wherein the eukaryotic cell is an insect cell.

CLMS (25)

25. The method of claim 20 wherein the host cell is a prokaryotic cell.

US PAT NO: 5,426,177 [IMAGE AVAILABLE] L1: 2 of 3  
DATE ISSUED: Jun. 20, 1995  
TITLE: Ciliary neurotrophic factor receptor  
INVENTOR: Samuel Davis, New York, NY  
Stephen P. Squinto, Irvington, NY  
Mark E. Furth, Pelham, NY  
George D. Yancopoulos, Briarcliff Manor, NY  
ASSIGNEE: Regeneron Pharmaceuticals, Inc., Tarrytown, NY (U.S. corp.)  
APPL-NO: 07/676,647  
DATE FILED: Mar. 28, 1991  
ART-UNIT: 182  
PRIM-EXMR: Robert J. Hill, Jr.  
ASST-EXMR: Sally P. Teng  
LEGAL-REP: Pennie & Edmonds

US PAT NO: 5,426,177 [IMAGE AVAILABLE] L1: 2 of 3

ABSTRACT:

The present invention relates to the ciliary neurotrophic factor (CNTF) receptor, and provides for CNTF receptor nucleic acid and amino acid sequences. It also relates to (i) assay systems for detecting CNTF activity; (ii) experimental model systems for studying the physiologic role of CNTF; (iii) diagnostic techniques for identifying CNTF-related neurologic conditions; (iv) therapeutic techniques for the treatment of CNTF-related neurologic and muscular conditions, and (v) methods for identifying molecules homologous to CNTF and CNTFR.

CLAIMS:

CLMS (1)

What is claimed is:

1. Isolated and purified CNTF receptor comprising the amino acid sequence as depicted in FIG. 2 (SEQ ID no. 1)

US PAT NO: 5,171,837 [IMAGE AVAILABLE] L1: 3 of 3  
DATE ISSUED: Dec. 15, 1992  
TITLE: Peptide capable of binding interleukin 6 and an adsorbent  
comprising the peptide immobilized on a carrier  
INVENTOR: Masao Tanihara, Kurashiki, Japan  
Kiichiro Oka, Kurashiki, Japan  
ASSIGNEE: Kuraray Co., Ltd., Okayama, Japan (foreign corp.)  
APPL-NO: 07/582,831  
DATE FILED: Oct. 5, 1990  
ART-UNIT: 184  
PRIM-EXMR: Robert A. Wax  
ASST-EXMR: Stephen Walsh  
LEGAL-REP: Wegner, Cantor, Mueller & Player

US PAT NO: 5,171,837 [IMAGE AVAILABLE] L1: 3 of 3

ABSTRACT:

A peptide being capable of binding to interleukin 6, and an adsorbent for interleukin 6 comprising the peptide immobilized on a carrier.

CLAIMS:

CLMS (1)

What is claimed is:

1. A peptide being capable of binding to interleukin 6 represented by the general formula:

H-X-A-Y-Z

wherein A is a peptide segment selected from the group consisting of  
a peptide segment of the formula: -Gly-Thr-Val-His-Leu-Leu-Val-Asp-Val-Pro-Pro-Glu-Glu-Pro-Gln-Leu-Ser-Cys-Phe-Arg-Lys-,  
a peptide segment of the formula: -Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-Phe-Gln-Glu-Pro-Cys-Gln-Tyr-Ser-Gln-Glu-Ser-,  
a peptide segment of the formula: -Thr-Ser-Leu-Pro-Gly-Asp-Ser-Val-Thr-Leu-Thr-Cys-Pro-Gly-Val-Glu-Pro-Glu-Asp-,  
a peptide segment of the formula: -Gln-Ala-Leu-Thr-Thr-Asn-Lys-Asp-Asp-Asp-Asn-Ile-Leu-Phe-Arg-Asp-Ser-Ala-,  
a peptide segment of the formula: -Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-,  
a peptide segment of the formula: -Ser-Thr-Pro-Ser-Leu-Thr-Thr-Lys-Ala-Val-Leu-Leu-Val-Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-,  
a peptide segment of the formula: -Asn-Pro-Arg-Trp-Leu-Ser-Val-Thr-Trp-Gln-Asp-Pro-His-Ser-,  
a peptide segment of the formula: -His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-

Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys,  
a peptide segment of the formula: -Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-,  
a peptide segment of the formula: -Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-,  
a peptide segment of the formula: -Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-, and  
a peptide segment of the formula: -Trp-Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-;  
each of X and Y is a single bond or an amino acid residue selected from the group consisting of Asp, Glu, Lys, Ala and a divalent group of the formula: -NH(CH<sub>2</sub>)<sub>n</sub>-CO- (wherein n is an integer of 1 to 17),  
or a peptide segment composed of 2 to 10 amino acid residues selected from the above group bound to each other through a peptide bond; and Z is a hydroxyl group or an amino group.

#### CLMS (2)

2. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Gly-Thr-Val-His-Leu-Leu-Val-Asp-Val-Pro-Pro-Glu-Glu-Pro-Gln-Leu-Ser-Cys-Phe-Arg-Lys-.

#### CLMS (3)

3. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-Phe-Gln-Glu-Pro-Cys-Gln-Tyr-Ser-Gln-Glu-Ser-.

#### CLMS (4)

4. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Thr-Ser-Leu-Pro-Gly-Asp-Ser-Val-Thr-Leu-Thr-Cys-Pro-Gly-Val-Glu-Pro-Glu-Asp-.

#### CLMS (5)

5. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Gln-Ala-Leu-Thr-Thr-Asn-Lys-Asp-Asp-Asp-Asn-Ile-Leu-Phe-Arg-Asp-Ser-Ala-.

#### CLMS (6)

6. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys.

#### CLMS (7)

7. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Ser-Thr-Pro-Ser-Leu-Thr-Thr-Lys-Ala-Val-Leu-Leu-Val-Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-.

#### CLMS (8)

8. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Asn-Pro-Arg-Trp-Leu-Ser-Val-Thr-Trp-Gln-Asp-Pro-His-Ser-.

#### CLMS (9)

9. A peptide according to claim 1, wherein A is a peptide segment of the formula: -His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys.

CLMS(10)

10. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS(11)

11. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS(12)

12. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS(13)

13. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Trp-Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS(14)

14. An adsorbent comprising the peptide according to claim 1 immobilized on a carrier.

CLMS(15)

15. An adsorbent comprising the peptide according to claim 2 immobilized on a carrier.

CLMS(16)

16. An adsorbent comprising the peptide according to claim 3 immobilized on a carrier.

CLMS(17)

17. An adsorbent comprising the peptide according to claim 4 immobilized on a carrier.

CLMS(18)

18. An adsorbent comprising the peptide according to claim 5 immobilized on a carrier.

CLMS(19)

19. An adsorbent comprising the peptide according to claim 6 immobilized on a carrier.

CLMS(20)

20. An adsorbent comprising the peptide according to claim 7 immobilized on a carrier.

CLMS(21)

21. An adsorbent comprising the peptide according to claim 8 immobilized on a carrier.

CLMS(22)

22. An adsorbent comprising the peptide according to claim 9 immobilized on a carrier.

CLMS(23)

23. An adsorbent comprising the peptide according to claim 10 immobilized on a carrier.

CLMS(24)

24. An adsorbent comprising the peptide according to claim 11 immobilized on a carrier.

CLMS(25)

25. An adsorbent comprising the peptide according to claim 12 immobilized on a carrier.

CLMS(26)

26. An adsorbent comprising the peptide according to claim 13 immobilized on a carrier.

```
=> ds
'DS' IS NOT A RECOGNIZED COMMAND
=> d his
      (FILE 'USPAT' ENTERED AT 10:35:38 ON 03 JUL 96)
L1      3 S HUMAN INTERLEUKIN 6 RECEPTOR?
=> s interleukin 6 receptor?
      2317 INTERLEUKIN
      1835874 6

      23249 RECEPTOR?
L2      12 INTERLEUKIN 6 RECEPTOR?
      (INTERLEUKIN(W) 6(W) RECEPTOR?)
=> s antibod?
L3      19922 ANTIBOD?
=> s l3 and l2
L4      12 L3 AND L2
=> d 1-12
```

1. 5,476,774, Dec. 19, 1995, Quantitation of nucleic acids using the polymerase chain reaction; Alice M. Wang, et al., 435/91.2, 6, 320.1; 536/24.33; 935/77, 78 [IMAGE AVAILABLE]

2. 5,470,730, Nov. 28, 1995, Method for producing T.sub.H -independent



cytotoxic T lymphocytes; Phillip D. Greenberg, et al., 435/172.3;  
424/93.21; 435/69.1, 69.52, 70.4, 252.3, 320.1 [IMAGE AVAILABLE]

3. 5,462,731, Oct. 31, 1995, Use of IL-6 for the treatment of chronic lymphocyte leukemia (CLL) and B-cell lymphomas; Dan Aderka, et al., 424/85.2, 85.1; 514/12, 21; 530/351 [IMAGE AVAILABLE]

4. 5,447,851, Sep. 5, 1995, DNA encoding a chimeric polypeptide comprising the extracellular domain of TNF receptor fused to IgG, vectors, and host cells; Bruce A. Beutler, et al., 435/69.7, 69.5, 240.2, 320.1; 530/300, 351; 536/23.4 [IMAGE AVAILABLE]

5. 5,426,177, Jun. 20, 1995, Ciliary neurotrophic factor receptor; Samuel Davis, et al., 530/395, 350, 839 [IMAGE AVAILABLE]

6. 5,326,559, Jul. 5, 1994, Treatment of accelerated atherosclerosis with interleukin-2 receptor targeted molecules; D. Douglas Miller, 424/85.2, 144.1, 183.1; 435/69.5, 69.52, 69.7, 70.21; 514/2, 8, 21, 824; 935/106, 107, 109 [IMAGE AVAILABLE]

7. 5,223,611, Jun. 29, 1993, DNA encoding for human GP130 protein; Tadimitsu Kishimoto, 530/351; 435/69.1, 320.1; 536/23.5 [IMAGE AVAILABLE]

8. 5,219,727, Jun. 15, 1993, Quantitation of nucleic acids using the polymerase chain reaction; Alice M. Wang, et al., 435/6, 91.2, 91.21; 536/24.33; 935/77, 78 [IMAGE AVAILABLE]

9. 5,216,128, Jun. 1, 1993, IFN-.beta.2/IL-6 receptor its preparation and pharmaceutical compositions containing it; Daniela Novick, et al., 530/350, 351, 413, 416, 834 [IMAGE AVAILABLE]

10. 5,188,828, Feb. 23, 1993, Interleukin-6 to stimulate erythropoietin production; Mark A. Goldberg, et al., 424/85.2; 514/8, 12; 530/351 [IMAGE AVAILABLE]

11. 5,171,837, Dec. 15, 1992, Peptide capable of binding interleukin 6 and an adsorbent comprising the peptide immobilized on a carrier; Masao Tanihara, et al., 530/324, 325, 326, 810 [IMAGE AVAILABLE]

12. 5,132,403, Jul. 21, 1992, Human gp130 protein; Tadimitsu Kishimoto, 530/351, 350, 388.22 [IMAGE AVAILABLE]

=>

> d his

(FILE 'USPAT' ENTERED AT 10:35:38 ON 03 JUL 96)

L1 3 S HUMAN INTERLEUKIN 6 RECEPTOR?

L2 12 S INTERLEUKIN 6 RECEPTOR?

L3 19922 S ANTIBOD?

L4 12 S L3 AND L2

=>

THE 1ST DEP. INTERNAL MED., NATL. DEFENCE MED. COLL., 3-2 NAMIKI, *Get*  
TOKOROZAWA, SAITAMA 359, JAPAN  
CLIN EXP IMMUNOL 88 (1). 1992 75-83. CODEN: CEXIA  
Full Journal Title: Clinical and Experimental Immunology  
Language: ENGLISH

Introducing avidin-biotin complex ELISA for anti-DNA antibody, the mechanism of in vitro production of anti-ssDNA antibody as well as of polyclonal immunoglobulin mediated by an IL-6-IL-6R loop was studied in patients with systemic lupus erythematosus (SLE). Regardless of the presence or absence of T cells, B cells from SLE patients could produce IgG anti-ssDNA antibody as well as total IgG without any stimulation. Low density B cells obtained by Percoll gradient density centrifugation responded to rIL-6 to produce IgG and IgG anti-ssDNA antibody. rIL-2 and rIL-4 had lesser effects on the differentiation of low density B cells. In fact, IL-6R was preferentially expressed on low density B cells from active SLE patients, as detected by anti-IL-6R MoAb, MT18, which did not inhibit IL-6 binding. SLE B cells, especially high density B cells, produced greater amounts of IL-6 in culture supernatants than did T cells, regardless of whether disease was active or inactive. Normal T cells and B cells did not produce significant amounts of IL-6. Thus, endogenous IL-6 produced by high density B cells bound to the IL-6R preferentially expressed on the low density B cells, and drove them into terminal differentiation, especially in active SLE patients. Further, addition of polyclonal anti-IL-6 or anti-IL-6R MoAb (PM1), which inhibited IL-6 binding, both inhibited IgG anti-ssDNA antibody as well as total IgG production by SLE B cells in a dose-dependent manner. These results suggest that interruption of the autocrine IL-6 loop would be of therapeutic value in SLE. ]

16/7/6  
DIALOG(R) File 55:BIOSIS PREVIEWS(R)  
(c) 1996 BIOSIS. All rts. reserv.

9032401 BIOSIS Number: 93017401  
ANTI-MURINE IL-6 RECEPTOR ANTIBODY INHIBITS IL-6 EFFECTS IN-VIVO  
SUZUKI H; YASUKAWA K; SAITO T; ANZAI M; GOITSUKA R; HASEGAWA A; OHSUGI Y;  
TAGA T; KISHIMOTO T  
INSTITUTE MOLECULAR CELLULAR BIOLOGY, OSAKA UNIV. 1-3, YAMADAOKA,  
SUITA-SHI, OSAKA 565, JAPAN.  
IMMUNOL LETT 30 (1). 1991 17-22. CODEN: IMLED  
Full Journal Title: Immunology Letters  
Language: ENGLISH

Thrombopoiesis, as well as antibody production, is one of the major events in which interleukin-6 (IL-6) has been reported to be involved. Polyclonal antimurine IL-6 receptor antibody was prepared to examine the effect of the antibody on these events in IL-6-treated mice. Administration of the anti-mIL-6R antibody inhibited the IL-6-induced increase in the number of platelets. Enhancement of the serum level of DNP-specific antibody by intraperitoneal injection of IL-6 was inhibited completely with simultaneous administration of the anti-mIL-6R antibody. The level of DNP-specific antibody was decreased, even below the basal value, by the higher dose of anti-mIL-6R antibody, indicating its effect also on endogenous IL-6. This work provides evidence that anti-IL-6R antibody inhibits IL-6 function in vivo, and provides an animal model of the therapeutic use of anti-IL-6R antibody for IL-6-related disease. ]

File 55:BIOSIS PREVIEWS(R) 1985-1996/Jun W4  
(c) 1996 BIOSIS

Set	Items	Description
---	-----	-----
?s il6		
S1	622	IL6
?s receptor?		
S2	301812	RECEPTOR?
?s interleukin(w) 6		
	78222	INTERLEUKIN
	621520	6
S3	12338	INTERLEUKIN (W) 6
?ds		

Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?
S3	12338	INTERLEUKIN (W) 6
?s s1 or s3		

	622	S1
	12338	S3
S4	12505	S1 OR S3
?s s4 and s2		

	12505	S4
	301812	S2
S5	2087	S4 AND S2
?s antibod?		

S6	259799	ANTIBOD?
?s s5 and s6		

	2087	S5
	259799	S6
S7	463	S5 AND S6
?s il(w) 6r		

	43566	IL
	1245	6R
S8	173	IL (W) 6R
?s s6 and s8		

	259799	S6
	173	S8
S9	64	S6 AND S8
?ds		

Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?

S3 12338 INTERLEUKIN(W) 6  
 S4 12505 S1 OR S3  
 S5 2087 S4 AND S2  
 S6 259799 ANTIBOD?  
 S7 463 S5 AND S6  
 S8 173 IL(W) 6R  
 S9 64 S6 AND S8  
 ?s interleukin(w) 6(w) receptor?

78222 INTERLEUKIN  
 621520 6  
 301812 RECEPTOR?  
 S10 281 INTERLEUKIN(W) 6(W) RECEPTOR?  
 ?s s6 and s10

259799 S6  
 281 S10  
 S11 63 S6 AND S10  
 ?s s9 or s11

64 S9  
 63 S11  
 S12 99 S9 OR S11  
 ?s py=(1993:1996)

S13 1717319 PY=(1993:1996)  
 ?s s12 not s13

99 S12  
 1717319 S13  
 S14 25 S12 NOT S13  
 ?s neutrali? or inhibit?

19962 NEUTRALI?  
 468055 INHIBIT?  
 S15 483053 NEUTRALI? OR INHIBIT?  
 ?s s14 and s15

25 S14  
 483053 S15  
 S16 12 S14 AND S15  
 ?t s16/7/1-12

16/7/1  
 DIALOG(R) File 55:BIOSIS PREVIEWS(R)  
 (c) 1996 BIOSIS. All rts. reserv.

10029465 BIOSIS Number: 95029465  
 ROLE OF INTERLEUKIN 6 IN THE GROWTH OF MYELOMA-DERIVED CELL LINES  
 BARUT B A; ZON L I; COCHRAN M K; PAUL S R; CHAUHAN D; MOHRBACHER A;  
 FINGEROTH J; ANDERSON K C  
 DIV. TUMOR IMMUNOL., DANA-FARBER CANCER INST., 44 BINNEY ST., BOSTON,  
 MASS. 02115.  
 LEUK RES 16 (10). 1992. 951-959. CODEN: LERED  
 Full Journal Title: Leukemia Research  
 Language: ENGLISH  
 The role of interleukin 6 (IL-6) in the growth of five multiple

myeloma-derived cell lines was characterized. The U266 and RPMI 8226 cells lines demonstrated increased DNA synthesis when cultured with exogenous IL-6, expressed IL-6 cell surface receptors (IL-6Rs) and expressed mRNA for IL-6R. However, these cells did not secrete detectable IL-6 protein, and a neutralizing antibody to IL-6 did not inhibit their growth. Three other myeloma-derived cells lines ARH-77, IM-9 and HS-Sultan did not respond to exogenous IL-6, secrete IL-6 or express cell surface IL-6Rs. The IL-6 responsive cell lines bore late B-cell surface antigens (Ags), CD38 and PCA-1, whereas those lines which were non-IL-6 responsive strongly expressed B1 (CD20) and B4 (CD19) Ags, representing earlier stages in B-cells differentiation. Finally, the two IL-6 responsive cell lines did not express Epstein-Barr virus (EBV) proteins; in contrast, EBV encoded proteins typically expressed during latency could be detected in the three non-IL-6 responsive lines, confirming infection with virus. These studies clarify the heterogeneity observed in the myeloma cell line phenotype and biology and suggest that the U266 and RPMI 8226 cells lines, which express IL-6 cell surface receptors and are IL-6 responsive, may be useful for further study of IL-6 signal transduction in and related IL-6 mediated growth of myeloma in vivo. In contrast, those cell lines which are IL-6-independent provide a model for further study of EBV transformation and IL-6-dependent growth mechanisms in malignancy.

16/7/2

DIALOG(R)File 55:BIOSIS PREVIEWS(R)  
(c) 1996 BIOSIS. All rts. reserv.

9787030 BIOSIS Number: 44037030

CLINICAL APPLICATIONS OF IL6 INHIBITORS

KLEIN B; LU Z Y; BATAILLE R

LAB. D'ONCOGENESE IMMUNOHEMATOL., INST. DE BIOL., 9 QUAI MONCOUSU, 44035  
NANTES, FR.

RES IMMUNOL 143 (7). 1992. 774-776. CODEN: RIMME

Full Journal Title: Research in Immunology

Language: ENGLISH

16/7/3

DIALOG(R)File 55:BIOSIS PREVIEWS(R)  
(c) 1996 BIOSIS. All rts. reserv.

9593256 BIOSIS Number: 94098256

ANTI-HUMAN INTERLEUKIN-6 RECEPTOR ANTIBODY INHIBITS HUMAN MYELOMA GROWTH  
IN-VIVO

SUZUKI H; YASUKAWA K; SAITO T; GOITSUKA R; HASEGAWA A; OHSUGI Y; TAGA T;  
KISHIMOTO T

DEP. MED. III, OSAKA UNIV. MED. SCH., 1-1-50 FUKUSHIMA, FUKUSHIMA-KU,  
OSAKA 553, JPN.

EUR J IMMUNOL 22 (8). 1992. 1989-1993. CODEN: EJIMA

Full Journal Title: European Journal of Immunology

Language: ENGLISH

Myeloma is one of the interleukin (IL)-6-related diseases to which abnormal expression of IL-6 has been reported to be linked. We examined the in vivo inhibitory effect of anti-human IL-6 receptor (IL-6R) antibody on human myeloma cell growth in mice. SCID mice were subcutaneously inoculated with solid tumor of the myeloma cell line S6B45 in which human IL-6 was acting as an autocrine growth factor. Ten intraperitoneal administrations of 100 .mu.g of the anti-human IL-6R antibody PM1 at 48-h intervals

strongly inhibited the growth of S6B45 cells when the administration started 24 h after tumor inoculation. The tumor growth inhibition in vivo was also observed by administration of the anti-human IL-6 antibody MH166 using the same procedure as for PM1. The inhibitory effect of PM1 was not significant when the administration started 5 or more days after tumor inoculation. This work indicates that anti-human IL-6R antibody, as well as anti-human IL-6 antibody inhibits human myeloma growth in vivo, and provides an animal model for testing the therapeutic value of agents such as antibodies to human IL-6, IL-6R and gp130, an IL-6R-associated signal transducer, in the treatment of human myelomas.

16/7/4

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

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9547472 BIOSIS Number: 94052472

INCREASE IN INTERLEUKIN 6 IL-6 AND IL-6 RECEPTOR EXPRESSION IN A HUMAN MULTIPLE MYELOMA CELL LINE U-266 DURING LONG-TERM IN-VITRO CULTURE AND THE DEVELOPMENT OF A POSSIBLE AUTOCRINE IL-6 LOOP

JERNBERG-WIKLUND H; PETTERSSON M; CARLSSON M; NILSSON K

LAB. TUMOR BIOLOGY, DEP. PATHOLOGY, UNIV. HOSP., S-751 85 UPPSALA, SWEDEN.

LEUKEMIA (BASINGSTOKE) 6 (4). 1992. 310-318. CODEN: LEUKE

Language: ENGLISH

A human multiple myeloma (MM) cell line, U-266, has developed the ability to grow independently of exogenous interleukin 6 (IL-6) during long-term cultivation in vitro. The early passage, feeder-cell dependent U-266 cell line (U-266-1970) was compared with the late passage U-266-1984 cell line with respect to response to IL-6, IL-1.beta. and tumour necrosis factor .alpha. and expression of IL-6 and IL-6 receptor (IL-6R) mRNA and protein. The results showed that; (a) only the U-266-1970 cell line was stimulated to growth by IL-6, (b) IL-6 and IL-6R mRNA were expressed in both cell lines, (c) the level of IL-6 mRNA was increased in the U-266-1984 cell line and only this line produced IL-6 and, (d) the level of IL-6R mRNA was highest in the U-266-1984 cell line and the number of IL-6R about ten times higher than in U-266-1970. The growth of the IL-6-producing U-266-1984 cell line was inhibited by 30% by anti-IL-6R antibodies suggesting the possibility that an autocrine IL-6 loop might have developed during the long-term cultivation. In addition to many other phenotypic alterations of the U-266 cell line, having developed as a consequence of tumor progression in vitro, its growth factor requirement seems to have evolved from a dependence on IL-6 as a paracrine growth factor to a capacity for autonomous growth, dependent on autocrine IL-6 stimulation. Whether such a development also may take place in MM clones in vivo remains to be established.

16/7/5

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

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9500353 BIOSIS Number: 94005353

AUTOSTIMULATORY EFFECTS OF IL-6 ON EXCESSIVE B CELL DIFFERENTIATION IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS ANALYSIS OF IL-6 PRODUCTION AND IL-6R EXPRESSION

KITANI A; HARA M; HIROSE T; HARIGAI M; SUZUKI K; KAWAKAMI M; KAWAGUCHI Y; HIDAKA T; KAWAGOE M; NAKAMURA H

16/7/7

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

8588351 BIOSIS Number: 92053351

PREPARATION OF SOLUBLE MURINE IL-6 RECEPTOR AND ANTI-MURINE II-6 RECEPTOR  
ANTIBODIES

SAITO T; YASUKAWA K; SUZUKI H; FUTATSUGI K; FUKUNAGA T; YOKOMIZO C;  
KOISHIHARA Y; FUKUI H; OHSUGI Y; ET AL

DIV. IMMUNOL., INST. MOL. CELL. BIOL., OSAKA UNIV., 1-3 YAMADA-OKA,  
SUITA-SHI, OSAKA 565, JPN.

J IMMUNOL 147 (1). 1991. 168-173. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

Starting with a previously isoalted cDNA clone encoding murine IL-6R, a stable transformed Chinese hamster ovary cell line constitutively expressing soluble murine IL-6R (smIL-6R) has been established. The smIL-6R was purified to homogeneity by sequential filtration and chromatography of culture medium. The smIL-6R augmented the sensitivity of M1 cells to IL-6 in their growth inhibition in a dose-response manner. Rat hybridomas producing mAb specific to murine IL-6R were also established. One of the clones, RS13, produced IgG2a isotype that was capable of inhibiting IL-6 activity. ELISA for the quantitation of smIL-6R was established, which could detect smIL-6R in a quantity as low as 1 ng/ml.

16/7/8

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

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8564429 BIOSIS Number: 92029429

IL-6 AND TUMOR NECROSIS FACTOR-ALPHA AUTOCRINE AND PARACRINE CYTOKINES  
INVOLVED IN B CELL FUNCTION

RIECKMANN P; D'ALESSANDRO F; NORDAN R P; FAUCI A S; KEHRL J H

LAB. IMMUNOREGULATION, NATIONAL INST. ALLERGY INFECTIOUS DISEASES, NIH,  
BUILDING 10, ROOM 11 B 13, BETHESDA, MD. 20892.

J IMMUNOL 146 (10). 1991. 3462-3468. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

IL-6 and TNF-.alpha. are synthesized and secreted by normal tonsillar B cells after stimulation with the polyclonal B cell activator Staphylococcus aureus Cowan strain 1 (SAC) and IL-2 as well as spontaneously by in vivo activated B cells from patients with hypergammaglobulinemia. Using specific neutralizing antibodies, both factors were shown to be involved in autocrine and/or paracrine regulation of B cell differentiation. IgG induced by SAC/IL-2 stimulation was reduced 73% with an anti-IL-6 antibody and 40% with an anti-TNF-.alpha. antibody. Similar effects of these antibodies were observed on the spontaneous in vitro IgG production by lymphoblastic B cells from six patients with hypergammaglobulinemia. Kinetic studies with SAC/IL-2-activated B cells revealed that the anti-TNF-.alpha. antibody must be present at the beginning of the culture to exert an effect on Ig production, whereas the anti-IL-6 antibody reduced Ig production even if added as late as day 3. This sequential action of TNF-.alpha. and IL-6 on B cell differentiation was reflected by different kinetics of release of these two cytokines into the supernatant of SAC/IL-2 activated B cells; TNF-.alpha. peaked at 24 h and IL-6 at 96 h after stimulation. In addition, it was shown that IL-6 production by in vitro-activated B cells was partially blocked by an anti-TNF-.alpha.



antibody suggesting that TNF-.alpha. regulates IL-6 production in normal B cells via an autocrine pathway. We also investigated the effects of TGF-.beta. on TNF-.alpha. and IL-6 production by normal B cells. Although TGF-.beta. inhibited Ig production by in vitro-activated and in vivo-activated B cells, it did not inhibit the release of these cytokines from normal B cells. Furthermore, TGF-.beta. did not inhibit the induction of nuclear factor-IL-6 nor the expression of IL-6R on activated B cells. Thus, although the biologic effects of anti-IL-6 and TGF-.beta. on B cell Ig production are similar, their mechanisms of actions appear to be distinct.

16/7/9

DIALOG(R)File 55:BIOSIS PREVIEWS(R)  
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8209434 BIOSIS Number: 91130434

CYTOKINE REGULATION OF LOCALIZED INFLAMMATION INDUCTION OF ACTIVATED B CELLS AND IL-6-MEDIATED POLYCLONAL IGG AND IGA SYNTHESIS IN INFLAMED HUMAN GINGIVA

KONO Y; BEAGLEY K W; FUJIHASHI K; MCGHEE J R; TAGA T; HIRANO T; KISHIMOTO T; KIYONO H

DEP. ORAL BIOLOGY, UNIVERSITY ALABAMA BIRMINGHAM, UAB STATION, BIRMINGHAM, ALA. 35294.

J IMMUNOL 146 (6). 1991. 1812-1821. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

It is well established that increased numbers of plasma cells occur in the localized tissues of chronic inflammatory diseases such as adult periodontitis, and enzymatic isolation has shown that most B lineage cells produce IgG-subclass with some IgA-subclass responses. It would be of importance to determine if excess production of cytokines in the localized lesion account for these responses and in the present study we have assessed gingival mononuclear cell (GMC) supernatants for cytokines that activate B cells including IL-6R expression and for levels of IL-6 present. Inasmuch as limited numbers (.apprx.1 to 3 .times. 10<sup>6</sup> cells) of GMC were obtained from surgically removed tissues (.apprx. 400 mg), we have focused on the analysis of IL-6 production by GMC in this study. Further, initial evidence of additional cytokines that are produced by GMC and induce expression of IL-6R on resting B cells has been obtained. The GMC and PBMC from individual patients were cultured in the presence (or absence) of Con A. Higher levels of IL-6 were produced spontaneously by GMC when compared with Con A-stimulated PBMC. When PBMC cultures were supplemented with GMC supernatants obtained from the same patient, high numbers of spot-forming cells (SFC), mainly in IgG followed by IgA isotype, were seen. The induction of SFC by GMC supernatants was inhibited by incubation with a goat anti-human IL-6 antibody. When the effect of GMC supernatants on subclasses of PBMC SFC was determined, the response was IgG1 > IgG2 > IgG3 = IgG4 and IgA1 > IgA2, a pattern remarkably similar to the distribution of plasma cells in the GMC itself. To assess for cytokines in GMC supernatants that mediated B cell activation, supernatants containing anti-IL-6 were cultured with PBMC or purified B cells for 72 h. This treatment induced small proliferative B cell responses and elevated expression of IL-6R on B cells, but did not induce SFC responses. Further, incubation of B cells with GMC supernatants induced resting B cells (G0/G1) to enter the cell cycle (S and G2/M). Addition of human rIL-6 to these cultures on day 3 restored IgG- and IgA-subclass SFC responses by day 7. Cytokine-induced IL-6R expression also occurred in vivo because freshly isolated GMC

expressed high levels of this receptor. These results show that GMC produce cytokines that induce B cell activation including IL-6R expression and secrete IL-6 that regulates B cell terminal differentiation into plasma cells of IgG- and IgA-subclasses. We are currently assessing the cytokines produced by GMC that induce the expression of IL-6R on B cells.

16/7/10

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

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8119517 BIOSIS Number: 91040517

INTERLEUKIN-6 IL-6 IS AN INTERMEDIATE IN IL-1-INDUCED PROLIFERATION OF  
LEUKEMIC HUMAN MEGAKARYOBLASTS

BRACH M A; LOWENBERG B; MANTOVANI L; SCHWULERA U; MERTELSMANN R; HERRMANN  
F

DEP. HEMATOLOGY ONCOLOGY, UNIVERSITY FREIBURG MEDICAL CENTER,  
HUGSTETTERSTRASSE 55, D-7800 FREIBURG, GER.

BLOOD 76 (10). 1990. 1972-1979. CODEN: BLOOA

Full Journal Title: Blood

Language: ENGLISH

We have examined the in vitro effects of recombinant human (rh) interleukin-1 (IL-1) on the growth of purified megakaryoblasts obtained from patients with acute megakaryoblastic leukemia. We demonstrate that both IL-1 alpha and IL-1 beta treatment of these cells led to stimulation of DNA synthesis (as shown by increase of 3H-thymidine incorporation up to 35-fold) and also resulted in colony formation of leukemic megakaryoblasts. However, the stimulatory effect of IL-1 was dependent on endogenous production of IL-6, because addition of neutralizing monoclonal antibody (MoAb) to IL-6 abrogated the stimulatory activity of IL-1. In contrast, neutralizing MoAbs to granulocyte (G)-colony stimulating factor (CSF), granulocyte-macrophage (GM)-CSF, and macrophage (M)-CSF failed to counteract the growth-enhancing effects of IL-1. Leukemic megakaryoblasts accumulated IL-6 mRNA and released IL-6 protein into their culture supernatant when exposed to rh IL-1 but failed to disclose transcripts for G-, GM-, and M-CSF under these conditions. Analysis of IL-6 receptor (IL-6R) transcript levels demonstrated that megakaryoblasts constitutively expressed IL-6R mRNA and that these transcripts are down-regulated to undetectable levels upon exposure to IL-1 and IL-6. Increase of 3H-thymidine incorporation by megakaryoblasts could be duplicated by exogenous IL-6 that could be blocked by neutralizing MoAb to IL-6. In conclusion, our results suggest that leukemic megakaryoblasts could produce and secrete IL-6, and express IL-6R, and that the growth-enhancing effect of IL-1 on these cells is indirect, via production of IL-6 by leukemic cells.

16/7/11

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

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7743486 BIOSIS Number: 90111486

ASSOCIATION BETWEEN IL-6 AND CD40 SIGNALING IL-6 INDUCES PHOSPHORYLATION  
OF CD-40 RECEPTORS

CLARK E A; SHU G

REG. PRIMATE RES. CENT. SJ-50, CENT HEALTH SCI., UNIV. WASHINGTON,  
SEATTLE, WA 98195.

J IMMUNOL 145 (5). 1990. 1400-1406. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

CD40 mAb at subsaturating doses inhibit the growth of transformants of the M12 murine cell line expressing intact full length CD40 molecules (M12/CD40+ cells) but do not inhibit the growth of two M12 transformants expressing either a mutant CD40 cDNA missing most of the cytoplasmic tail (CD40/tailless) or a mutant cDNA with a substitution at residue 234 (CD40/23A, Ala for Thr). Using these transformants, we tested a panel of cytokines for the ability to mimic CD40 mAb. rIL-6 behaved like CD40 mAb and inhibited the growth of M12/CD40+ cells but not of CD40/tailless or CD40/234A mutants. The effect of IL-6 on M12/CD40+ cells not only required intact CD40 including threonine 234 but also was specific because IL-6 mAb blocked the inhibitory activity. The M12/CD40+ cells responsive to IL-6 expressed > 300,000 CD40 molecules/cells but, like M12/CD40-controls, expressed only small numbers (<50/cell) of high affinity IL-6R, indicating that CD40 is not a receptor for IL-6. Nevertheless, IL-6 utilizes intact CD40 efficiently when it signals these cells: treatment of M12/CD40+ cells with IL-6 induced increased phosphorylation of CD40. Conversely, triggering CD40 on M12/CD40+ cells leads to IL-6 production. Similar effects were evident in human CD40+ B cells: IL-6 increased the phosphorylation of CD40 in the IL-6-responsive cell line, CESS, and CD40 mAb induced IL-6 production in activated human B cells. Thus, CD40 may function to receive and regulate IL-6-dependent signals in B cells.

16/7/12

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

7364057 BIOSIS Number: 89015076

CHARACTERIZATION OF IL-6 RECEPTOR EXPRESSION BY MONOCLONAL AND POLYCLONAL ANTIBODIES

HIRATA Y; TAGA T; HIBI M; NAKANO N; HIRANO T; KISHIMOTO T

DIV. IMMUNOL., INST. MOL. CELL. BIOL., OSAKA UNIV., 1-3 YAMADA-OKA,

SUITA, OSAKA 565, JPN.

J IMMUNOL 143 (9). 1989. 2900-2906. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

mAb and polyclonal antibodies against human IL-6R were prepared by using a murine transfectant cell line expressing the human IL-6R and a synthetic oligopeptide made on the basis of the deduced amino acid sequence as immunogens. Immunoprecipitation of radiolabeled IL-6R with these antibodies showed that the Mr of a mature IL-6R was 80 kDa and its value was reduced to 50K after treatment with O- and N-glycanase and neuraminidase, indicating that IL-6R is a glycoprotein. Two mAb recognizing different epitopes were prepared. One, PM1 inhibited the binding of 125I-IL-6 to the receptor and blocked the IL-6-dependent growth of a T lymphoma line, KT3. PM1 could not bind to IL-6R when it was saturated with IL-6, indicating that this antibody recognizes the IL-6 binding or the adjacent site on IL-6R. The other, MT18 was not inhibited by IL-6R, therefore, this could be used for cytofluorometric staining of normal cells. Nonstimulated B cells expressed undetectable amount of IL-6R regardless of the expression of surface IgD. However, after the stimulation with PWM, IL-6R was observed on IgD- B cells with a relatively large size, but subtly on IgD- small B cells and not on IgD+ B cells, fitting the function of IL-6 which acts on activated B cells to induce Ig production. In contrast, IL-6R was detected on non-stimulated CD4+/CD8- and CD4-/CD8+ T cells. The level of IL-6R on both T cell subpopulations was not significantly changed after stimulation

with phytohemagglutinin.  
?s human(w)il(w)6(w)receptor?

```
      2371757  HUMAN
      43566   IL
      621520   6
      301812   RECEPTOR?
S17      30   HUMAN(W) IL(W) 6 (W) RECEPTOR?
```

?ds

Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?
S3	12338	INTERLEUKIN(W) 6
S4	12505	S1 OR S3
S5	2087	S4 AND S2
S6	259799	ANTIBOD?
S7	463	S5 AND S6
S8	173	IL(W) 6R
S9	64	S6 AND S8
S10	281	INTERLEUKIN(W) 6 (W) RECEPTOR?
S11	63	S6 AND S10
S12	99	S9 OR S11
S13	1717319	PY=(1993:1996)
S14	25	S12 NOT S13
S15	483053	NEUTRALI? OR INHIBIT?
S16	12	S14 AND S15
S17	30	HUMAN(W) IL(W) 6 (W) RECEPTOR?

?s s6 and s17

```
      259799  S6
      30      S17
S18      13   S6 AND S17
?s chimeric or humaniz? or reshap?
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      8485   CHIMERIC
      442   HUMANIZ?
      185   RESHAP?
S19      9024 CHIMERIC OR HUMANIZ? OR RESHAP?
?s s18 and s19
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      13     S18
      9024   S19
S20      1   S18 AND S19
?t s20/7/1
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20/7/1  
DIALOG(R)File 55:BIOSIS PREVIEWS(R)  
(c) 1996 BIOSIS. All rts. reserv.

11039162 BIOSIS Number: 97239162

Humanization of a mouse anti-human interleukin-6 receptor antibody  
comparing two methods for selecting human framework regions

Sato K; Tsuchiya M; Saldanha J; Koishihara Y; Ohsugi Y; Kishimoto T;  
Bendig M M

Chugai Pharm. Co. Ltd., Fuji-Gotemba Res. Labs, 1-135 Komakado,

Gotemba-shi, Shizuoka 412, JAP

Molecular Immunology 31 (5). 1994. 371-381.

Full Journal Title: Molecular Immunology

ISSN: 0161-5890

Language: ENGLISH

Print Number: Biological Abstracts Vol. 097 Iss. 011 Ref. 156275

Mouse monoclonal antibody AUK12-20 binds to human IL-6 receptor and inhibits IL-6 functions. It has been humanized by CDR-grafting for therapeutic use. In the design of reshaped human AUK12-20 V-L region, the human framework regions (FRs) from the human Bence-Jones protein REI were used. The reshaped human AUK12-20 light chain, in combination with chimeric AUK12-20 heavy chain, bound to antigen as well as chimeric AUK12-20 antibody. In the design of reshaped human AUK12-20 V-H region, two sets of the human FRs were chosen and compared. One set was from the consensus amino acid sequence for human V-H regions subgroup (HSG)-I and the other set was from human antibody HAX, the most similar human V-H region found in a database of human immunoglobulin sequences. The HSG-I-based and the HAX-based reshaped human AUK12-20 heavy chains in combination with the reshaped human AUK12-20 light chain, showed approximately 90 and 100% antigen-binding and competition-binding activities as compared to the chimeric or mouse AUK12-20 heavy chains. Most importantly, these humanized antibodies inhibited the IL-6-dependent tumor cell growth as well as the original mouse antibody suggesting that these humanized antibodies could be efficacious in human patients. Our results show that both approaches for the design of reshaped human antibodies can be used for successful humanization. The approach based on FRs from the most similar individual human antibody, however, seemed to be best for designing a reshaped human antibody that mimicked as closely as possible the original mouse antibody.

?ds

Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?
S3	12338	INTERLEUKIN(W) 6
S4	12505	S1 OR S3
S5	2087	S4 AND S2
S6	259799	ANTIBOD?
S7	463	S5 AND S6
S8	173	IL(W) 6R
S9	64	S6 AND S8
S10	281	INTERLEUKIN(W) 6 (W) RECEPTOR?
S11	63	S6 AND S10
S12	99	S9 OR S11
S13	1717319	PY=(1993:1996)
S14	25	S12 NOT S13
S15	483053	NEUTRALI? OR INHIBIT?
S16	12	S14 AND S15
S17	30	HUMAN(W) IL(W) 6 (W) RECEPTOR?
S18	13	S6 AND S17
S19	9024	CHIMERIC OR HUMANIZ? OR RESHAP?
S20	1	S18 AND S19

?s s10 and s6 and s19

	281	S10
	259799	S6
	9024	S19
S21	2	S10 AND S6 AND S19

?t s21/7/1-2

21/7/1

DIALOG(R)File 55:BIOSIS PREVIEWS(R)  
(c) 1996 BIOSIS. All rts. reserv.

11039162 BIOSIS Number: 97239162

Humanization of a mouse anti-human interleukin-6 receptor antibody  
comparing two methods for selecting human framework regions

Sato K; Tsuchiya M; Saldanha J; Koishihara Y; Ohsugi Y; Kishimoto T;  
Bendig M M

Chugai Pharm. Co. Ltd., Fuji-Gotemba Res. Labs, 1-135 Komakado,  
Gotemba-shi, Shizuoka 412, JAP

Molecular Immunology 31 (5). 1994. 371-381.

Full Journal Title: Molecular Immunology

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Mouse monoclonal antibody AUK12-20 binds to human IL-6 receptor and inhibits IL-6 functions. It has been humanized by CDR-grafting for therapeutic use. In the design of reshaped human AUK12-20 V-L region, the human framework regions (FRs) from the human Bence-Jones protein REI were used. The reshaped human AUK12-20 light chain, in combination with chimeric AUK12-20 heavy chain, bound to antigen as well as chimeric AUK12-20 antibody. In the design of reshaped human AUK12-20 V-H region, two sets of the human FRs were chosen and compared. One set was from the consensus amino acid sequence for human V-H regions subgroup (HSG)-I and the other set was from human antibody HAX, the most similar human V-H region found in a database of human immunoglobulin sequences. The HSG-I-based and the HAX-based reshaped human AUK12-20 heavy chains in combination with the reshaped human AUK12-20 light chain, showed approximately 90 and 100% antigen-binding and competition-binding activities as compared to the chimeric or mouse AUK12-20 heavy chains. Most importantly, these humanized antibodies inhibited the IL-6-dependent tumor cell growth as well as the original mouse antibody suggesting that these humanized antibodies could be efficacious in human patients. Our results show that both approaches for the design of reshaped human antibodies can be used for successful humanization. The approach based on FRs from the most similar individual human antibody, however, seemed to be best for designing a reshaped human antibody that mimicked as closely as possible the original mouse antibody.

21/7/2

DIALOG(R)File 55:BIOSIS PREVIEWS(R)  
(c) 1996 BIOSIS. All rts. reserv.

10110788 BIOSIS Number: 95110788

RESHAPING A HUMAN ANTIBODY TO INHIBIT THE INTERLEUKIN 6-DEPENDENT TUMOR  
CELL GROWTH

SATO K; TSUCHIYA M; SALDANHA J; KOISHIHARA Y; OHSUGI Y; KISHIMOTO T;  
BENDIG M M

FUJI-GOTEMBA RESEARCH LAB., CHUGAI PHARMACEUTICAL CO. LTD., 1-135  
KOMAKADO, GOTEMBA, SHIZUOKA 412, JPN.

CANCER RES 53 (4). 1993. 851-856. CODEN: CNREA

Full Journal Title: Cancer Research

Language: ENGLISH

The mouse PM-1 monoclonal antibody binds to the human interleukin 6

receptor, inhibits IL-6 functions, and shows strong antitumor cell activity against multiple myeloma cells. In order to be effective as a therapeutic agent administered to human patients in repeated doses, reshaped human PM-1 antibodies consisting of human REI-based light chain and NEW-based heavy chain variable regions were designed and constructed with the assistance of a structural model of the mouse PM-1 variable regions. The best reshaped human PM-1 antibody is equivalent to mouse or chimeric PM-1 antibody in terms of antigen binding and growth inhibition against multiple myeloma cells. Only a few minor changes in the human framework regions were required to recreate the mouse PM-1 antigen-binding site within a human antibody. The reshaped human PM-1 antibody, therefore, could be efficacious in human multiple myeloma patients.

?s pm(w)1

21795 PM

1252383 1

S22 278 PM(W)1

?s s6 and s22

259799 S6

278 S22

S23 24 S6 AND S22

?t s23/7/1-23

23/7/1

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

12222771 BIOSIS Number: 98822771

Purification and characterization of salivary kallikrein from an insectivore (*Scalopus aquaticus*): Substrate specificities, immunoreactivity and kinetic analyses

Richards G P; Zintz C; Chao J; Chao L

Med. Univ. South Carolina, Dep. Biochemistry Molecular Biol., 171 Ashley Ave., Charleston, SC 29425, USA

Archives of Biochemistry and Biophysics 329 (1). 1996. 104-112.

Full Journal Title: Archives of Biochemistry and Biophysics

ISSN: 0003-9861

Language: ENGLISH

Print Number: Biological Abstracts Vol. 101 Iss. 012 Ref. 173193

We report the successful one-step separation of tissue kallikrein from the salivary glands of an insectivore, the Eastern Atlantic mole (*Scalopus aquaticus*) by perfusion chromatography. Purified mole salivary kallikrein was characterized as a 30-kDa serine proteinase with a pI of 5.3 and a pH optimum of 9.0. It was readily recognized by human tissue kallikrein antibody in immunoblot analyses. It preferentially hydrolyzes fluorogenic peptidyl substrates with arginyl residues, rather than lysyl residues at the P1 substrate recognition site, indicating that it is like other mammalian kallikreins. Mole kallikrein efficiently releases kinin from low molecular weight human, dog, and bovine kininogen substrates with specific activities similar to that of human tissue kallikrein. Steady state kinetics performed with the synthetic tripeptidyl substrates, Phe-Phe-Arg-, Pro-Phe-Arg-, and Val-Leu-Arg-7-amino-4-methylcoumarin, gave K-m values for mole kallikrein of 3.3, 46.1, and 2.8  $\mu$ -M, respectively, and specificity constants, k-cat/K-m, of 3818, 165, and 8714 s<sup>-1</sup> pM<sup>-1</sup>, respectively. Mole kallikrein, when compared with human and rat tissue kallikreins, more closely resembles human kallikrein based on immunoreactivity and

kininogenase activity. Mole kallikrein appears to be a member of a single gene or small multigene family. *S. aquaticus* is recommended for studying the evolution of mammalian proteins and may offer advantages over rodent models for biomedical research.

23/7/2

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

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12032670 BIOSIS Number: 98632670

Two consecutive nucleotide substitutions resulting in the T3 receptor beta gene resulting in an 11-amino acid truncation in a patient with generalized resistance to thyroid hormone

Miyoshi Y; Nakamura H; Sasaki S; Tagami T; Misaki T; Konishi J; Nakao K  
2nd Div., Dep. Internal Med., Hamamatsu Univ. Sch. Med., 3600 Hamadacho,  
Hamamatsu 431-31, Japan

Molecular and Cellular Endocrinology 114 (1-2). 1995. 9-17.

Full Journal Title: Molecular and Cellular Endocrinology

ISSN: 0303-7207

Language: ENGLISH

Print Number: Biological Abstracts Vol. 101 Iss. 004 Ref. 048415

We identified unusual mutations in the T3 receptor (TR) beta gene in a 6-year-old Japanese girl with generalized resistance to thyroid hormone. Two consecutive base substitutions, T to A and C to A at nucleotide positions 1637 and 1638, respectively, changed the 451st codon coding for Phe(TTC) to stop codon (TAA), resulting in an 11-amino acid carboxyl(C)-terminus truncation. The patient was a heterozygote. Western blotting using an anti-TR antibody demonstrated the truncated receptor protein. The patient showed severe mental retardation (IQ41), disturbance in speech development, and attention deficit hyperactivity disorder. Thyroid functional status by clinical evaluation was considered within the normal range in spite of high serum thyroid hormone levels (T4 725.9 nmol/l, T3 12.7 nmol/l, FT4 166.0 pmol/l). TSH increased from 0.6 to 24 mU/L after TRH (150 mu-g) injection. TSH secretion as well as 123I-uptake was suppressed only partially by T3 (75 mu-g/day for a week). Close examination of thyroid functions and TR-beta gene analysis were not possible in the family, except for paternal grandmother and one of her two sisters who showed no abnormality. The patient's truncated TR-beta showed very low T3 binding activity ( $K_a = 0.1$  times  $10^{-10}$  M), transcriptional activity, and a very strong dominant negative effect. When co-expressed with wild-type TR-beta at the molar ratio 1:1 in CV-1 cells, the mutant receptor inhibited the wild-type TR-beta transcriptional activity by 74% at 10 nM T3. Even 1 mu-M T3 could not normalize these impaired functions.

23/7/3

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

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11772862 BIOSIS Number: 98372862

The regulatory site of functional GTP binding protein coupled to the high affinity cholecystokinin receptor and phospholipase A-2 pathway is on the G-beta subunit of G-q protein in pancreatic acini

Tsunoda Y; Owyang C

Dep. Internal Med., Univ. Mich., Ann Arbor, MI 48109, USA

Biochemical and Biophysical Research Communications 211 (2). 1995.

648-655.



Full Journal Title: Biochemical and Biophysical Research Communications

ISSN: 0006-291X

Language: ENGLISH

Print Number: Biological Abstracts Vol. 100 Iss. 005 Ref. 064700

A non-hydrolysable guanosine nucleotide analog, GTP(S) at 200  $\mu$ M, stimulated amylase secretion which was inhibited by an anti-phospholipase A-2 (PLA-2) antibody in permeabilized pancreatic acini, indicating that the PLA-2 pathway is linked to the GTP binding protein. A high affinity cholecystokinin (CCK) receptor agonist, CCK-OPE (10  $\mu$ M), and a low affinity receptor agonist, CCK-8 (0.1  $\mu$ M), both caused amylase secretion in permeabilized cells. The action of CCK-OPE was abolished by the GB antibody but not by the G- $\alpha$ -q,11 antibody, whereas the opposite was true of the CCK-8 response. Biscoclaurine alkaloid isotetrandrine (10  $\mu$ M), a specific inhibitor of PLA-2-coupled G proteins, abolished Ca-2+ oscillations and amylase secretion induced by CCK-OPE (0.1100 nM), but not by CCK-8 (10 pM) in intact acini. Gp antagonist-2A (10  $\mu$ M), which inhibits the activation of Gq, also inhibited the actions of CCK-OPE (10 pM-1  $\mu$ M) in intact acini. These observations indicate that the functional unit of the heterotrimeric G protein coupled to the high affinity CCK receptor appears to be different from that linked to the low affinity CCK receptor/G-q- $\alpha$  pathway. The regulatory site of this G protein coupled to the high affinity CCK receptor is on the beta subunit of G-q protein which elicits Ca-2+ oscillations and monophasic amylase secretion via the PLA-2 pathway.

23/7/4

DIALOG(R) File 55:BIOSIS PREVIEWS(R)

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11490979 BIOSIS Number: 98090979

Subclinical hypothyroidism resulting from autoimmune thyroiditis in female patients with endogenous depression

Custro N; Scafidi V; Lo Baido R; Nastri L; Abbate G; Cuffaro M P; Gallo S ; Vienna G; Notarbartolo A

Cattedra di Patologia Medica, Via del Vespro 141, 90127 Palermo, Italy

Journal of Endocrinological Investigation 17 (8). 1994. 641-646.

Full Journal Title: Journal of Endocrinological Investigation

ISSN: 0391-4097

Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 005 Ref. 061389

Thyroid function and presence of thyroid autoantibodies were assessed in a group of 75 consecutive female patients with mood disturbances and in a group of 38 healthy women of similar age recruited as controls. Nine patients suffered from major (endogenous) depression and 66 from minor (neurotic) depression. The individual patients had normal values of circulating thyroid hormones. Nevertheless, endogenously depressed patients had total serum triiodothyronine ( $M \pm SE = 1.49 \pm 0.09$  nmol/l) and both total ( $83.9 \pm 4.3$  nmol/l) and free serum thyroxine ( $13.9 \pm 1.1$  pmol/l) lower than in the group of minor depressed and in the group of controls ( $p < 0.01$ , in both comparison). The median value of serum thyrotropin was 5.22 mU/l in the major depressed patients versus 1.72 mU/l in the minor depressed and 1.69 mU/l in the controls. Thyroid function test results in the minor depressed group did not significantly differ from those in the controls. Five of the 9 endogenously depressed patients were subclinically hypothyroid, while none of the 66 patients with minor depressive disorder showed thyroid dysfunction. Antibodies against thyroglobulin and/or thyroid peroxidase were positive in all the 5 endogenously depressed women with

subclinical hypothyroidism, revealing a symptomless autoimmune thyroiditis, which was also confirmed by ultrasonography in all cases and histopathologically demonstrated in one case. None of the endogenously depressed women without thyroid dysfunction and none of the 66 minor depressives were seropositive for thyroid autoantibodies. Only one of the non-depressed women in the control group was found seropositive for TPO-Ab and showed an exaggerated TSH responsiveness to TRH stimulation. The findings indicate the possibility that endogenous depression is accompanied by latent hypothyroidism in an appreciable proportion of women. The detection of thyroid autoantibodies in such patients suggests that affective disorders might play a precipitating role in the development of thyroid autoimmune disease. Therefore, the possibility of immunological damage should be taken into consideration whenever depressed women display biochemical thyroid dysfunction.

23/7/5

DIALOG(R) File 55:BIOSIS PREVIEWS(R)  
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11413460 BIOSIS Number: 98013460

Transforming growth factor beta 2 is the predominant isoform in the neural retina, retinal pigment epithelium-choroid vitreous of the monkey eye

Pfeffer B A; Flanders K C; Guerin C J; Danilepour D; Anderson D H  
Storz Div. American Cyanamid, Build. 96, Room 225A, 401 N. Middletown  
Road, Pearl River, NY 10965, USA

Experimental Eye Research 59 (3). 1994. 323-333.

Full Journal Title: Experimental Eye Research

ISSN: 0014-4835

Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 001 Ref. 013460

Several techniques were utilized to assess the levels, disposition and cellular sources of isoforms 1 and 2 of transforming growth factor beta (TGF-beta) in the posterior pole of the monkey eye. Freshly dissected tissues, as well as the saline vehicles in which dissections were performed, were analysed by sandwich enzyme-linked immunosorbent assay. In all tissues TGF-beta-2 was the predominant isoform, with beta-2:beta-1 ratios of 6: 1 for neural retina (as ng g-1) and 425:1 for vitreous (as pmol 1-1). Retinal pigment epithelium (RPE)-Bruch's membrane-choroid complex contained approximately 10 times the amount of both TGF-beta isoforms as neural retina. For first passage cultures of monkey RPE, TGF-beta-2, but not TGF-beta-1, accumulated over time in conditioned media samples. Immunoreactivity for TGF-beta-2 was detected both in tissue sections of posterior pole, specifically in rod outer segments and RPE, and also in the first passage cultures of RPE. Antibodies to specific peptide sequences of both isoforms localized TGF-beta to the outer segments of rod photoreceptors. The apparent sequestration of TGF-beta-2 in photoreceptor outer segments, as well as the in vitro evidence for possible synthesis and release by RPE, suggest that TGF-beta-2 is an important modulator of visual function acting at the retina-RPE interface.

23/7/6

DIALOG(R) File 55:BIOSIS PREVIEWS(R)  
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11249497 BIOSIS Number: 97449497

Cryptic nature of envelope V3 region epitopes protects primary monocytotropic human immunodeficiency virus type 1 from antibody neutralization

Bou-Habib D C; Roderiquez G; Oravec T; Berman P W; Lusso P; Norcross M A  
Div. Hematol. Products, Center Biol. Evaluation Res., Food Drug  
Administration, NIH, Building 29A, Room 3B10, 8800 Rockville Pike, HFM-541,  
Bethesda, MD 20892, USA

Journal of Virology 68 (9). 1994. 6006-6013.

Full Journal Title: Journal of Virology

ISSN: 0022-538X

Language: ENGLISH

Print Number: Biological Abstracts Vol. 098 Iss. 008 Ref. 103809

Characterization of biological and immunological properties of human immunodeficiency virus type 1 (HIV-1) is critical to developing effective therapies and vaccines for AIDS. With the use of a novel CD4+ T-cell line (PM-1) permissive to infection by both monocytotropic (MT) and T-cell-tropic virus types, we present a comparative analysis of the immunological properties of a prototypic primary MT isolate of HIV-1 strain JR-CSF (MT-CSF) with those of a T-cell-tropic variant (T-CSF) of the same virus, which emerged spontaneously in vitro. The parental MT-CSF infected only PM-1 cells and was markedly resistant to neutralization by sera from HIV-1-infected individuals, rabbit antiserum to recombinant MT-CSF gp120, and anti-V3 monoclonal antibodies. The T-CSF variant infected a variety of CD4+ T-cell lines, contained positively charged amino acid substitutions in the gp120 V3 region, and was highly sensitive to antibody neutralization. Neutralization and antibody staining of T-CSF-expressing cells were significantly inhibited by HIV-1 V3 peptides; in contrast, the MT strain showed only weak V3-specific binding of polyclonal and monoclonal antibodies. Exposure of PM-1 cells to a mixture of both viruses in the presence of human anti-HIV-1 neutralizing antiserum resulted in infection with only MT-CSF. These results demonstrate that although the V3 region of MT viruses is immunogenic, the target epitopes in the V3 principal neutralizing domain on the membrane form of the MT envelope appear to be cryptic or hidden from blocking antibodies.

23/7/7

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

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10930136 BIOSIS Number: 97130136

Direct and correlated responses to multitrait, divergent selection for immunocompetence

Kean R P; Cahaner A; Freeman A E; Lamont S J

Dep. Animal Sci., Iowa State Univ., Ames, IA 50011, USA

Poultry Science 73 (1). 1994. 18-32.

Full Journal Title: Poultry Science

ISSN: 0032-5791

Language: ENGLISH

Print Number: Biological Abstracts Vol. 097 Iss. 006 Ref. 079999

Leghorn lines had been selected for an immunocompetence index based on four traits: antibody production to Mycoplasma gallisepticum (MG) and Pasteurella multocida (PM) vaccines, reticuloendothelial clearance of colloidal carbon (CCA), and cell-mediated, wing web response to phytohemagglutinin (PHA). The purpose of this study was to produce replicated lines of chickens with divergent levels of multitrait immunocompetence by index selection. The objectives of analyses of Generations 5 to 7 of this study was to characterize these lines with

respect to immune-response traits, correlations among these traits, and correlated responses in other important production traits. Differences (P lt .05) existed between the lines selected for high or low immune response and between the two replicates in mean breeding values and in individual immune-response traits. Averages of heritability estimates, weighted by number of offspring and pooled across three generations (two cycles of selection), estimated by using sire variance components and parent-offspring correlations were, respectively, .16 and .09 for the index, .31 and .08 for MG, .21 and -.02 for PM, .06 and .05 for CCA, and .08 and .12 for PHA. Realized heritabilities (response divided by effective selection differential) pooled across the two selection cycles, were .19 and .11 for the index, .06 and -.01 for MG, .44 and .32 for PM, 1.52 and -1.21 for CCA, and .48 and .15 for PHA, for Replicates 1 and 2, respectively. Phenotypic correlations among traits were generally small, and several estimates were negative. Estimates of genetic correlation varied widely. Juvenile and adult body weights, age of first egg, 32-wk egg weight, and rate of egg production were analyzed to evaluate effects of selection on these traits of direct economic importance. Very few differences were noted.

23/7/8

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10110788 BIOSIS Number: 95110788

RESHAPING A HUMAN ANTIBODY TO INHIBIT THE INTERLEUKIN 6-DEPENDENT TUMOR CELL GROWTH

SATO K; TSUCHIYA M; SALDANHA J; KOISHIHARA Y; OHSUGI Y; KISHIMOTO T;  
BENDIG M M

FUJI-GOTEMBA RESEARCH LAB., CHUGAI PHARMACEUTICAL CO. LTD., 1-135  
KOMAKADO, GOTEMBA, SHIZUOKA 412, JPN.

CANCER RES 53 (4). 1993. 851-856. CODEN: CNREA

Full Journal Title: Cancer Research

Language: ENGLISH

The mouse PM-1 monoclonal antibody binds to the human interleukin 6 receptor, inhibits IL-6 functions, and shows strong antitumor cell activity against multiple myeloma cells. In order to be effective as a therapeutic agent administered to human patients in repeated doses, reshaped human PM-1 antibodies consisting of human REI-based light chain and NEW-based heavy chain variable regions were designed and constructed with the assistance of a structural model of the mouse PM-1 variable regions. The best reshaped human PM-1 antibody is equivalent to mouse or chimeric PM-1 antibody in terms of antigen binding and growth inhibition against multiple myeloma cells. Only a few minor changes in the human framework regions were required to recreate the mouse PM-1 antigen-binding site within a human antibody. The reshaped human PM-1 antibody, therefore, could be efficacious in human multiple myeloma patients.

23/7/9

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10098735 BIOSIS Number: 95098735

DEVELOPMENT OF MONOCLONAL ANTIBODIES SPECIFIC FOR 1 N-2  
ETHENODEOXYGUANOSINE AND N-2 3 ETHENODEOXYGUANOSINE AND THEIR USE FOR  
QUANTITATION OF ADDUCTS IN G12 CELLS EXPOSED TO CHLOROACETALDEHYDE

FOILES P G; MIGLIETTA L M; NISHIKAWA A; KUSMIEREK J T; SINGER B; CHUNG  
F-L  
DIV. CHEM. CARCINOGENESIS, AMERICAN HEALTH FOUND., ONE DANA RD.,  
VALHALLA, NY 10595, USA.

CARCINOGENESIS (OXF) 14 (1). 1993. 113-116. CODEN: CRNGD

Language: ENGLISH

Monoclonal antibodies specific for N2,3-ethenodeoxyguanosine (N2,3-.epsilon.dGuo) and 1,N2-ethenodeoxyguanosine (1,N2-.epsilon.dGuo) were developed. In a competitive ELISA, 50% inhibition of binding of the N2,3-.epsilon.dGuo specific antibody (ETH1) was achieved with 18 fmol of N2,3-.epsilon.dGuo. Fifty per cent inhibition of the 1,N2-.epsilon.dGuo-specific antibody (ETH2) required 11 pmol 1,N2-.epsilon.dGuo. Immunoassays for N2,3-.epsilon.dGuo and 1,N2-.epsilon.dGuo in single-stranded DNA were developed using these antibodies. The immunoassays could detect as little as 48 fmol of N2,3-.epsilon.dGuo or 340 fmol 1,N2-.epsilon.dGuo in 25 .mu.g of single stranded DNA. These assays and previously developed immunoassays for 1,N6-ethenodeoxyadenosine (1,N6-.epsilon.dAdo) and 3,N4-ethenodeoxycytidine (3,N4-.epsilon.dCyd) were used to measure etheno adduct levels in DNA of cells exposed to chloroacetaldehyde. The cells used were V79 cells with an inactivated hprt gene and a single copy of the bacterial gpt gene (G12 cells). The most abundant etheno adduct was 1,N6-.epsilon.dAdo, followed by 3,N4-.epsilon.dCyd and N2,3-.epsilon.dGuo. 1,N2-.epsilon.dGuo was not detected in chloroacetaldehyde-treated G12 cells. Chloroacetaldehyde was also shown to be mutagenic in these same cells.

23/7/10

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10020207 BIOSIS Number: 95020207

INCREASED TISSUE CONCENTRATIONS OF THE GASTRIN PRECURSOR IN PATIENTS  
TREATED WITH OMEPRAZOLE

NEMETH J; VARRO A; BRIDSON J; WALKER R; DOCKRAY G J

DEP. PHYSIOL., UNIVERSITY LIVERPOOL, CROWN ST., PO BOX 147, LIVERPOOL L69  
3BX, UK.

EUR J CLIN INVEST 22 (10). 1992. 638-644. CODEN: EJCIB

Full Journal Title: European Journal of Clinical Investigation

Language: ENGLISH

The main form of gastrin in antral mucosa, the amidated heptadecapeptide G17, is generated from an inactive precursor, progastrin, by steps involving endopeptidase cleavage and amidation. Gastrin cells are normally inhibited by gastric acid and in this study we have examined how suppression of acid by treatment with omeprazole for 6-8 weeks influences gastrin production in patients with oesophagitis. Plasma concentrations of total amidated gastrins in the fasting state increased from 18 to 43 pmol l<sup>-1</sup>; assays specific for G17-immunoreactivity indicated that the plasma concentrations of this form increased from 6 to 12 pmol l<sup>-1</sup>. In endoscopic biopsies of antral mucosa there was no change with omeprazole treatment in the concentrations of total amidated gastrins, or their immediate precursors, the Gly-extended gastrins. However, assays using an antibody that reacts with progastrin, together with size exclusion chromatography, indicated that tissue progastrin concentration increased 6-fold. The data suggest a modest net increase in gastrin production with omeprazole-treatment; because the ratio of tissue concentrations of total amidated gastrins to Gly-extended gastrins did not change, it would seem that the amidating capacity of the gastrin cell was maintained. However,

the increase in progastrin concentrations suggests a relative failure of the initial steps of post-translational processing, and consequently that in certain circumstances endopeptidase cleavage of progastrin may be rate limiting.

23/7/11

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9143686 BIOSIS Number: 93128686

TROPHOBLAST-DERIVED TUMOR NECROSIS FACTOR-ALPHA INDUCES RELEASE OF HUMAN CHORIONIC GONADOTROPIN USING INTERLEUKIN-6 IL-6 AND IL-6-RECEPTOR-DEPENDENT SYSTEM IN THE NORMAL HUMAN TROPHOBLASTS

LI Y; MATSUZAKI N; MASUHIRO K; KAMEDA T; TANIGUCHI T; SAJI F; YONE K; TANIZAWA O

1-1-50 FUKUSHIMA, FUKUSHIMA-KU, OSAKA 553, JPN.

J CLIN ENDOCRINOL METAB 74 (1). 1992. 184-191. CODEN: JCEMA

Full Journal Title: Journal of Clinical Endocrinology & Metabolism

Language: ENGLISH

The titer of tumor necrosis factor-.alpha. (TNF.alpha.) secreted by placental blocks was determined by enzyme immunoassay. The source of placental TNF.alpha. was immunohistochemically demonstrated with monoclonal anti-TNF.alpha. antibody to be only trophoblasts. Purified trophoblasts produced 174.4 ng/L TNF.alpha. by 24 h of culture in vitro. To investigate the role of TNF.alpha. in placental hormonogenesis, purified trophoblasts were stimulated with recombinant TNF.alpha. (rTNF.alpha.) to determine the hCG titer by enzyme immunoassay. Trophoblasts stimulated with rTNF.alpha. released hCG in a dose-dependent fashion with kinetics similar to those of recombinant interleukin-1 (rIL-1)-stimulated trophoblasts. The stimulated trophoblasts released IL-6 before hCG, but failed to show hCG release when pretreated with anti-IL-6 receptor (anti-IL-6R) monoclonal antibody PM-1. However, the pretreatment of trophoblasts with PM-1 did not interfere with rTNF-.alpha.-induced IL-6 release, ruling out the possibility of a nonspecific toxic effect of PM-1 on trophoblasts. These results suggest that trophoblast-derived TNF.alpha. induced IL-6 release and then activated the IL-6 -R system in trophoblasts to release hCG. Since IL-1 has also been demonstrated to induce similar release of IL-6 and hCG from trophoblasts, the effects of TNF.alpha. and IL-1 on these trophoblast functions were also examined. Simultaneous stimulation of trophoblasts with rTNF.alpha. and .gamma.IL-1.alpha. resulted in synergistic enhancement of IL-6 release, subsequently leading to enhanced hCG release. Collectively, trophoblast-derived TNF.alpha. and IL-1 synergistically regulated the level of IL-6 secreted by trophoblasts, the magnitude of which determined the level of hCG released by activating the IL-6-R system in trophoblasts.

23/7/12

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9113449 BIOSIS Number: 93098449

RADIO-IMMUNOASSAY OF ENDOTHELIN IN HUMAN PLASMA

SORENSEN S S

DEP. NEPHROLOGY MED. C, SKEJBY HOSP., DK-8200 AARHUS C, DENMARK.

SCAND J CLIN LAB INVEST 51 (7). 1991. 615-623. CODEN: SJCLA

Full Journal Title: Scandinavian Journal of Clinical and Laboratory Investigation

Language: ENGLISH

Endothelin (ET) is a newly described endothelium-derived 21-amino-acid peptide with potent vasoconstrictive properties. The present study describes a radio-immunoassay utilizing an antibody without cross-reactivity with big endothelin, produced after immunization of rabbits with endothelin-1 (ET-1). Measurement of endothelin in human plasma was performed after prior extraction on Sep-pak C18 cartridges. Recovery of unlabelled endothelin-1 added to human plasma (3.5 pg ml<sup>-1</sup>) was 84.8  $\pm$  11.1% (mean  $\pm$  SD, n = 12). The minimum detectable level in plasma was 50 fmol l<sup>-1</sup>. High-pressure liquid chromatography on reverse-phase C18 column established that the measured irET eluted identically to ET-1. The concentration of irET in plasma from healthy control subjects was 1.11  $\pm$  0.2 pmol l<sup>-1</sup> (mean  $\pm$  SD, n = 30). Agarose electrophoresis of plasma with [125I]-ET-1 indicated a reversible binding to albumin. It is concluded that ET-1 is present in measurable amounts in human plasma. It is suggested that ET-1 in plasma is associated with albumin. The importance of an adequate extraction procedure is stressed.

23/7/13

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9112746 BIOSIS Number: 93097746

DETERMINATION OF PLASMA CHOLECYSTOKININ CCK CONCENTRATIONS BY BIOASSAY AND RADIOIMMUNOASSAY IN MAN A CRITICAL EVALUATION

HOECKER M; SCHMIDT W E; CREUTZFELDT W; CHOUDHURY A R; NUSTEDE R; SCHAFFMAYER A; FOELSCH U R

DIVISION GASTROENTEROLOGY ENDOCRINOLOGY, DEP. MEDICINE, UNIVERSITY HOSPITAL, GEORG-AUGUST-UNIVERSITY GOETTINGEN, ROBERT-KOCH-STRASSE 40, D-3400 GOETTINGEN, GER.

REGUL PEPT 37 (3). 1992. 255-269. CODEN: REPPD

Full Journal Title: Regulatory Peptides

Language: ENGLISH

The present investigation was designed to perform a direct comparison of a rat pancreatic acini bioassay system and a specific CCK radioimmunoassay (antiserum G-160) for the measurement of fasting and meal-stimulated plasma CCK in the presence and absence of the CCK receptor antagonist loxiglumide. The G-160 CCK antiserum is directed against the C-terminal O-sulfated tyrosine residue of the CCK molecule which is essential for full bioactivity of CCK peptides. For plasma extraction prior to bioassay measurement, hydrophobic reverse-phase chromatography on octadecylsilane cartridges was employed and resulted in simultaneous adsorption and elution of both CCK peptides and loxiglumide with recoveries of 87.5  $\pm$  9% and 75.0  $\pm$  5.9%, respectively. In the absence of loxiglumide, fasting and meal-stimulated values for CCK-like bioactivity and CCK-immunoreactivity (IR-CCK) were nearly identical (basal values: 1-2 pmol/l; meal-stimulated plateau levels; 4-6 pmol/l). After intravenous infusion of loxiglumide (30 mg/kg/h for 10 min, 10 mg/kg/h thereafter), resulting in plasma steady state levels of 200-300  $\mu$ mol/l, meal-stimulated CCK-like bioactivity was undetectable, whereas IR-CCK levels were augmented 6.5-fold. In the bioassay system, standard samples containing 50  $\mu$ mol/l loxiglumide produced complete inhibition of acinar lipase release in response to 50 pmol/l synthetic CCK-8. We conclude, that postprandial circulating non-CCK-like factors do not contribute significantly to the direct receptor-mediated stimulation of exocrine pancreatic secretion. The good agreement of CCK-like bioactivity and IR-CCK levels in the absence of loxiglumide confirms the sensitive and specific recognition of bioactive



CCK peptides by the G-160 antiserum and suggests that this antibody exerts binding characteristics probably similar to a pancreatic acinar receptor.

23/7/14

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9020358 BIOSIS Number: 93005358

EARLY UNDIFFERENTIATED CONNECTIVE TISSUE DISEASE II. THE FREQUENCY OF CIRCULATING ANTINUCLEAR ANTIBODIES IN PATIENTS WITH EARLY RHEUMATIC DISEASES

CLEGG D O; WILLIAMS H J; SINGER J Z; STEEN V D; SCHLEGEL S; ZIMINSKI C; ALARCON G S; LUGGEN M E; POLISSON R P; ET AL

DIV. RHEUMATOL., ROOM 4B 200, UNIV. UTAH MED. CENT., 50 NORTH MEDICAL DRIVE, SALT LAKE CITY, UTAH 84132.

J RHEUMATOL 18 (9). 1991. 1340-1343. CODEN: JRHUA

Full Journal Title: Journal of Rheumatology

Language: ENGLISH

The presence of antinuclear antibodies (ANA) in the serum is a common finding in various connective tissue disorders, but usefulness of these antibodies in making diagnoses or prognoses is not known. We report the results of a panel of ANA determinations including ANA, anti-dsDNA, Sm, RNP, SSA, SSB, Jo-1, Scl-70 and PM-1 in 410 patients in a 5-year descriptive study of 410 patients with rheumatic disease symptoms of less than one year's duration. While some patients met diagnostic criteria for a specific rheumatologic diagnosis, others were classified as undifferentiated connective tissue disease (UCTD) and were subclassified by a constellation of symptoms. Our results show that ANA is sensitive in systemic lupus erythematosus (SLE) and progressive systemic sclerosis even in early disease but is not specific. Other "specific" autoantibodies were seen most frequently in SLE but were relatively insensitive and were seen in low frequency in UCTD. ANA have limited diagnostic value in patients with early disease. The prognostic value of these tests will be assessed as the prospective study of these cohorts progresses.

23/7/15

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8085593 BIOSIS Number: 91006593

PARADOXICAL ENHANCEMENT OF INTERLEUKIN-2-MEDIATED CYTOTOXICITY AGAINST K562 CELLS BY ADDITION OF A LOW DOSE OF METHOTREXATE

NAKARAI T; UENO Y; UENO Y; KOIZUMI S

DEP. PEDIATRICS, KANAZAWA UNIV. SCH. MED., 13-1 TAKARA-MACHI, KANAZAWA 920, JAPAN.

CANCER IMMUNOL IMMUNOTHER 32 (1). 1990. 8-12. CODEN: CIIMD

Full Journal Title: Cancer Immunology Immunotherapy

Language: ENGLISH

In vitro effects of methotrexate (MTX) on interleukin-2(IL-2)-mediated cytotoxicity of peripheral blood mononuclear cells (PBMC) were studied. PBMC were incubated with human recombinant IL-2 (25 U/ml) for 72 h; during the last 24 h, various concentrations (10 pM-1  $\mu$ M) of MTX were added to the culture. Cytotoxicity against k562 cells was measured by a 4-h <sup>51</sup>Cr-release assay. The IL-2-mediated cytotoxicity was paradoxically increased at around a concentration (10 nM) MTX. Such a low concentration of MTX showed no anti-proliferative effect on cell growth. This enhancement



with 10 nM MTX was shown only in an E-rosette+ (E+) population, but not in E-rosette- (E-). In addition, when E+ cells were treated with an anti-CD16 monoclonal antibody plus complement after incubation with IL-2 and MTX, MTX-induced enhancement was lost, suggesting that an E+CD16+ cell population was mainly involved in this augmentation. Positively sorted E+CD16+ cells showed similar enhancement of cytotoxicity after treatment with IL-2 plus MTX. On the other hand, MTX treatment did not show the phenotypical changes including of the E+CD16+ cells, indicating that this treatment did not affect the differentiation and proliferation of the specific cell subset. Our results indicate that a low dose of MTX could have a role in the regulation of immunological anti-cancer surveillance systems through the natural killer and lymphokine-activated cytotoxic cells.

23/7/16

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7729928 BIOSIS Number: 90097928

TROPHOBLAST-DERIVED INTERLEUKIN-6 IL-6 REGULATES HUMAN CHORIONIC GONADOTROPIN RELEASE THROUGH IL-6 RECEPTOR ON HUMAN TROPHOBLASTS

NISHINO E; MATSUZAKI N; MASUHIRO K; KAMEDA T; TANIGUCHI T; TAKAGI T; SAJI F; TANIZAWA O

DEP. OBSTETRICS GYNECOLOGY, OSAKA UNIVERSITY MEDICAL SCHOOL, 1-1-50 FUKUSHIMA, FUKUSHIMA-KU, OSAKA 553, JPN.

J CLIN ENDOCRINOL METAB 71 (2). 1990. 436-441. CODEN: JCEMA

Full Journal Title: Journal of Clinical Endocrinology & Metabolism

Language: ENGLISH

We examined the capacity of trophoblast-derived interleukin-6 (IL-6) to stimulate secretion of placental hormones, including hCG. IL-6 stimulated hCG secretion by trophoblasts to a level similar to that stimulated by a GnRH analog. The analog, however, released hCG by an IL-6-independent mechanism because PM-1, a monoclonal antibody specific for IL-6 receptors (R), failed to block GnRH-mediated responses, but completely blocked IL-6 mediated hCG secretion, suggesting the existence of two distinct regulatory pathways for hCG release. Immunohistochemical analysis with another IL-6-R-specific antibody, MT-18, showed that IL-6-R was located only on the trophoblast layer of the placenta. Our data revealed the existence of a local regulatory network by which trophoblast-derived IL-6 interacts with IL-6-R on the trophoblasts, resulting in hCG release. Thus, two different regulatory networks, an IL-6 and IL-6-R system and a GnRH and GnRH-R system, regulate hCG release by human trophoblasts independently.

23/7/17

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7692329 BIOSIS Number: 90060329

MOLECULAR VARIANTS OF CHOLECYSTOKININ AFTER ENDOGENOUS STIMULATION IN HUMANS A TIME STUDY

EYSSELEIN V E; EBERLEIN G A; HESSE W H; SCHAEFFER M; GRANDT D; WILLIAMS R ; GOEBELL H; REEVE J R JR

DEP. GASTROENTEROL., HARBOR-UCLA MED. CENT., 1000 W. CARSON, ST., TORRANCE, CALIF. 90509.

AM J PHYSIOL 258 (6 PART 1). 1990. G951-G957. CODEN: AJPHA

Full Journal Title: American Journal of Physiology

Language: ENGLISH

The time-dependent release of molecular variants of cholecystokinin (CCK) into the circulation was studied before and 1, 2, and 4 h after a test meal in six healthy volunteers. At each time period, 100 ml of blood were drawn in a manner to inhibit CCK degradation. Plasma was formed and CCK concentrated by Sep-Pak C18 cartridge chromatography. Molecular variants of CCK and gastrin were well separated from each other by high-performance liquid chromatography (HPLC). Molecular forms of CCK and gastrin were measured by radioimmunoassay using an antibody that requires the presence of the carboxyl-terminal phenylalanine amide for full recognition, implying that biologically active forms were detected. HPLC elution positions of gastrin forms were determined using a gastrin-specific antibody. Chromatographic separation of CCK from gastrin forms was complete, allowing separate integration of gastrin and CCK forms. Therefore no subtraction of gastrin-like immunoreactivity from CCK-like immunoreactivity (CCK-LI) was necessary and CCK-LI could be directly determined. Peaks of CCK-LI were integrated in the column eluates and the plasma concentrations were calculated. Total plasma CCK-LI rose from a value of 2.4  $\pm$  0.6 pM before the test meal to 6.4  $\pm$  0.8, 6.6  $\pm$  0.9, and 5.8  $\pm$  1.2 pM 1, 2, and 4 h postprandially. The major molecular forms released into the circulation eluted on HPLC in the position of CCK-58 and CCK-39 (which coelutes with CCK-33). Minor amounts were detected in the position of CCK-8. There was no significant difference in the relative proportions of the molecular forms released at the different time periods. The high proportions of CCK-58 in human plasma indicate that it expresses a major portion of CCK's biological activity.

23/7/18

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7398030 BIOSIS Number: 89049049

DETECTION AND ANTIGENIC CHARACTERIZATION OF ANTINUCLEAR ANTIBODIES IN CONNECTIVE TISSUE DISEASES

DE MARNEFFE P; MALAISE M; DEFLANDRE E; HAUWAERT C; LALLEMAND M P; FRANCHIMONT P

SERV. RHUMATOLOGIE, CHU SART TILMAN, LIEGE.

REV MED LIEGE 44 (19). 1989. 577-591. CODEN: RMLIA

Full Journal Title: Revue Medicale de Liege

Language: FRENCH

To determine the correlation between the presence of antinuclear antibodies (ANA) and connective tissue disease, a prospective clinical study was conducted on 167 patients with one of the following conditions: systemic lupus erythematosus (SLE), induced lupus, rheumatoid arthritis, scleroderma, mixed connective tissue disease, primary Sjogren's syndrome, dermatomyositis, combined SLE and scleroderma, and psoriatic arthritis. ANA in patients' serum were detected and titrated by indirect immunofluorescence, and the pattern of immunofluorescence (homogeneous, peripheral, speckled, nucleolar, centromeric or chromosomal) was noted; ANA were characterized using the "nDNA C. L. Sci. Medx", "ENA antigen system" and "ANA check" kits from Biolab SA. Serum ANA were found to include antibodies to native DNA (anti-DNA), deoxyribonucleoprotein (anti-DNP), and extractable nuclear antigens (anti-ENA); included in the last group were anti-Smith antibodies (anti-Sm), antibodies to ribonucleoprotein (anti-U1-RNP), and the antibodies to Ro/SS-A, La/SS-B, Scl-70, Jo-1, PM-1, Ku, centromere and nucleolus. Some ANA were found to be specific for certain diseases, e.g. anti-DNA for lupus, anti-Sm for SLE, anti-Scl-70 and

anticentromere for scleroderma. Other antibodies, although not specific, were frequently associated with diseases, e.g. anti-RNP with SLE, anti-Ro/SS-A and anti-La/SS-B with Sjogren's syndrome. Detection and characterization of ANA was concluded to be of prognostic value and could be used as a diagnostic tool and an aid in treatment planning.

23/7/19

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6944784 BIOSIS Number: 87005305

EFFECT OF INTERLEUKIN 1 BETA ON TRANSDUCING MECHANISMS IN 235-1 CLONAL PITUITARY CELLS PART II MODULATION OF CALCIUM FLUXES

SCHETTINI G; MEUCCI O; FLORIO T; SCALA G; LANDOLFI E; GRIMALDI M  
DEP. PHARMACOL., II SCH. MED., VIA PANSINI 5, 80131 NAPOLI, ITALY.

BIOCHEM BIOPHYS RES COMMUN 155 (3). 1988. 1097-1104. CODEN: BBRCA

Full Journal Title: Biochemical and Biophysical Research Communications

Language: ENGLISH

In the present study we investigated the effect of the interleukin 1 beta on intracellular free calcium concentrations in 235-1 cell line both in basal conditions and after stimulation by the calcium channel activator maitotoxin. Interleukin 1 beta (from 0.01 pM to 10 nM) was unable to significantly affect basal cytosolic free calcium levels in acute conditions. The preincubation of these cells with interleukin 1 beta for 48h modulates maitotoxin stimulation of calcium fluxes without modifying basal intracellular free calcium levels. Low concentrations of interleukin 1 beta (0.01 pM, 1 pM) caused a marked reduction of intracellular free calcium concentrations increase induced by maitotoxin while higher doses of the monokine potentiated maitotoxin stimulation of calcium fluxes. The specificity of interleukin 1 beta effect was tested by means of polyclonal anti-interleukin 1 beta antibody (titer 1:100) which significantly abolished the inhibitory effect of interleukin 1 beta on free cytosolic calcium levels. These results show that a long lasting interaction of interleukin 1 beta with its receptor is able to influence voltage-sensitive calcium channels activation induced by maitotoxin in 235-1 cells.

23/7/20

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6638080 BIOSIS Number: 86104631

ENHANCED HUMAN MONOCYTE CYTOTOXICITY BY PLATELET-ACTIVATING FACTOR

VALONE F H; PHILIP R; DEBS R J

DEP. MED., VA MED. CENTER, SAN FRANCISCO, CA 94143, USA.

IMMUNOLOGY 64 (4). 1988. 715-718. CODEN: IMMUA

Full Journal Title: Immunology

Language: ENGLISH

The capacity of platelet-activating factor (PAF) to enhance human monocyte cytotoxicity for WEHI 164 cells was examined. Spontaneous monocyte cytotoxicity was 24 .+- . 2% (mean .+- . SEM, n =9). Preincubation of monocytes with 1 pM-1 nM PAF for 18 hr significantly enhanced cytotoxicity in a dose-related manner, whereas less enhancement was observed at PAF concentrations above 1 nM. Maximal PAF-induced cytotoxicity was 68 .+- . 6%, which was similar to that induced by optimal concentrations of tumour necrosis factor (TNF) and interferon-gamma. The specific PAF antagonist kadsurenone inhibited PAF-induced cytotoxicity but not TNF-induced

cytotoxicity. The inactive PAF analogues lysoPAF and enantioPAF did not increase monocyte cytotoxicity. Two observations suggest that TNF mediates PAF-induced cytotoxicity: specific anti-TNF antibodies inhibited PAF induced cytotoxicity toward WEHI 164 cells, and PAF did not enhance cytotoxicity to TNF-resistant cells. PAF represents a distinct class of phospholipid monocyte activators that increase monocyte cytotoxicity by TNF-dependent mechanisms.

23/7/21

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

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5427916 BIOSIS Number: 82072719

SMALL NUCLEAR RIBONUCLEOPROTEIN ANTIGENS ARE ABSENT FROM 10S TRANSLATION INHIBITORY RIBONUCLEOPROTEIN BUT PRESENT IN CYTOPLASMIC MESSENGER RIBONUCLEOPROTEIN AND POLYSOMES

BOAK A M; KOVACS S A; AGRIS P F; CHAKRABORTY D; SARKAR S

DEP. MED. DIV. BIOL. SCI., UIV. MISSOURI, COLUMBIA, MO. 65211.

ARCH BIOCHEM BIOPHYS 248 (1). 1986. 89-100. CODEN: ABBIA

Full Journal Title: Archives of Biochemistry and Biophysics

Language: ENGLISH

A cytoplasmic 10S ribonucleoprotein particle (iRNP), which is isolated from chick embryonic muscle, is a potent inhibitor of mRNA translation in vitro and contains a 4S translation inhibitory RNA species (iRNA). The iRNP particle shows similarity in size to the small nuclear ribonucleoprotein (snRNP) particles. Certain autoimmune disease patients contain antibodies directed against snRNP antigenic determinants. The possibility that iRNP may be related to the small nuclear particles was tested by immunoreactivity with monospecific autoimmune antibodies to six antigenic determinants (Sm, RNP, PM-1, SS-A (Ro), SS-B (La), and Scl-70). By Ouchterlony immunodiffusion assays, the cytoplasmic 10S iRNP did not show any immunoreactivity. Also, a more sensitive hemagglutination inhibition assay for detecting Sm and RNP antigens failed to show reactivity with the 10S iRNP. Thus, the 10S iRNP particles are distinct from the similarly sized snRNP. However, free and polysomal messenger ribonucleoprotein (mRNP) particles and polysomes also isolated from chick embryonic muscle and analyzed by Ouchterlony immunodiffusion and hemagglutination inhibition for the presence of the antigenic determinants showed reactivity to Sm and RNP autoantibodies, but were not antigenic for the other four antibodies. Some of the Sm antigenic peptides of mRNP particles and polysomes were identical to those purified from calf thymus nuclear extract, as judged by Western blot analysis. The association of Sm with free and polysomal mRNP and polysomes suggests that Sm may be involved in some cytoplasmic aspects of mRNA metabolism, in addition to a nuclear function in mRNA processing.

23/7/22

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4853405 BIOSIS Number: 79095720

IMMUNOGENETIC STUDIES OF JUVENILE DERMATOMYOSITIS 3. STUDY OF ANTIBODY TO ORGAN-SPECIFIC AND NUCLEAR ANTIGENS

PACHMAN L M; FRIEDMAN J M; MARYJOWSKI-SWEENEY M L; JONNASON O; RADVANY R M; SHARP G C; COBB M A; BATTLES N D; CROWE W E; ET AL

DIV. IMMUNOLOGY/RHEUMATOLOGY, CHILDREN'S MEMORIAL HOSPITAL, 2300 CHILDREN'S PLAZA, CHICAGO, IL 60614.

ARTHRITIS RHEUM 28 (2). 1985. 151-157. CODEN: ARHEA

Full Journal Title: Arthritis and Rheumatism

Language: ENGLISH

Children (90) with definite juvenile dermatomyositis (JDMS), who had been HLA typed, were tested for the presence of tissue or organ-specific antibodies. Sixty had active disease at the time of study. The mean disease duration was 4 yr and 30 had soft tissue calcifications. The following autoantibodies were sought: thyroid, gastric parietal cells, smooth muscle, striated muscle, microsomes, mitochondria, DNA, extractable nuclear antigen, Sm, PM-1, antinuclear antibody (ANA) and rheumatoid factor. Only the ANA and PM-1 were more frequent in patients than in controls ( $P < 0.0002$  and  $P < 0.001$ , respectively). Higher levels of immune complexes ( $P < 0.01$ ) were in sera from patients with JDMS than in sera from controls and were correlated with the presence of ANA in patients ( $P < 0.01$ ). Soft tissue calcification was not associated with any autoantibody or HLA antigen, but with disease duration and activity ( $P < 0.001$  and  $P < 0.05$ , respectively). There was no association between the occurrence of any autoantibody and the presence of HLA-B8 or DR3 among the white patients with JDMS. The frequency of autoantibodies in 43 full siblings of children with JDMS was not increased. Children with JDMS, with or without HLA-B8/DR3, do not show evidence of a generalized nonspecific antibody response to tissue antigens. The significance of the increased antibody to nuclear antigens ANA and PM-1 remains to be determined.

23/7/23

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4836297 BIOSIS Number: 79078612

HIGH-AFFINITY MONOCLONAL ANTIBODIES FOR AFLATOXINS AND THEIR APPLICATION TO SOLID-PHASE IMMUNOASSAYS

GROOPMAN J D; TRUDEL L J; DONAHUE P R; MARSHAK-ROTHSTEIN A; WOGAN G N  
BOSTON UNIVERSITY SCHOOL PUBLIC HEALTH, HUBERT H. HUMPHREY CANCER  
RESEARCH CENTER, DEPARTMENT MICROBIOLOGY, SCHOOL MEDICINE, 80 EAST CONCORD  
STREET, BOSTON, MASS. 02118.

PROC NATL ACAD SCI U S A 81 (24). 1984 (RECD. 1985). 7728-7731.

CODEN: PNASA

Full Journal Title: Proceedings of the National Academy of Sciences of the United States of America

Language: ENGLISH

Monoclonal antibodies specific for aflatoxin B1, aflatoxin B2, aflatoxin M1 and the major aflatoxin-DNA adducts were obtained following fusion of mouse SP-2 myeloma cells with spleen cells of mice immunized with aflatoxin B1 covalently bound to bovine gamma globulin. The aflatoxin-modified protein used to immunize mice was produced chemically by activating aflatoxin B1 to a 2,3-epoxide derivative, which then covalently bound to the protein. One of the monoclonal antibodies isolated (2B11) was a high-affinity IgM antibody with an affinity constant for aflatoxin B1, aflatoxin B2 and aflatoxin M1 of .apprx. 1 .times. 109 l/mol. In a competitive radioimmunoassay using [3H]aflatoxin B1, 3 pmol (1 ng) of aflatoxin B1, aflatoxin B2 or aflatoxin M1 caused 50% inhibition with this antibody. The antibody also had significant cross-reactivity for the major aflatoxin-DNA adducts: 2,3-dihydro-2-(N7-guanyl)-3-hydroxyaflatoxin B1 and 2,3-dihydro-2-(N5-formyl-2',5',6'-triamino-4' oxo-N5-pyrimidyl)-3-hydroxyaflatoxin B1. The antibody was also covalently bound to Sepharose-4B and used in a column-based solid-phase immunosorbent assay system. Aflatoxins added in vitro to phosphate buffer, human urine, human serum or human milk at

levels expected to be obtained in human samples acquired from environmentally exposed individuals were quantitatively recovered by applying the mixture to this antibody affinity column purification system. Preliminary studies using urine samples from rats injected with radiolabeled aflatoxin B1 have also indicated that aflatoxin metabolites can be isolated by these methods. The monoclonal antibody affinity columns can be regenerated for multiple use. Therefore, the monoclonal antibodies and their application to affinity chromatography represents a useful and rapid technique to purify environmentally occurring levels of this carcinogen and some of its metabolites for quantitative measurements.

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Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?
S3	12338	INTERLEUKIN(W) 6
S4	12505	S1 OR S3
S5	2087	S4 AND S2
S6	259799	ANTIBOD?
S7	463	S5 AND S6
S8	173	IL(W) 6R
S9	64	S6 AND S8
S10	281	INTERLEUKIN(W) 6 (W) RECEPTOR?
S11	63	S6 AND S10
S12	99	S9 OR S11
S13	1717319	PY=(1993:1996)
S14	25	S12 NOT S13
S15	483053	NEUTRALI? OR INHIBIT?
S16	12	S14 AND S15
S17	30	HUMAN(W) IL(W) 6 (W) RECEPTOR?
S18	13	S6 AND S17
S19	9024	CHIMERIC OR HUMANIZ? OR RESHAP?
S20	1	S18 AND S19
S21	2	S10 AND S6 AND S19
S22	278	PM(W) 1
S23	24	S6 AND S22

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